

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 06:47:29 ; Search time 8799 Seconds  
(without alignments)  
7873.651 Million cell updates/sec

Title: US-10-017-867A-281  
Perfect score: 2320  
Sequence: 1 agggtccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
	1	1180.4	50.9	1182	29	AY404343 Homo sapi
	2	912.2	39.3	2197	11	AK050128 Mus muscu
	3	857.4	37.0	1180	29	AY404344 Pan trogl
	4	853.2	36.8	879	13	BQ216829 AGENCOURT
	5	738	31.8	916	14	CD050395 AGENCOURT
	6	733.8	31.6	1185	29	AY404345 Mus muscu
	7	731.6	31.5	1353	11	AK041045 Mus muscu
	8	522.4	22.5	978	12	BI102968 602888578
	9	488.6	21.1	761	12	BI559553 603252894
c	10	463.6	20.0	694	10	AW173071 xj82g11.x
c	11	457.6	19.7	659	14	CB435346 615435 MA
	12	452.6	19.5	1723	11	AK052644 Mus muscu
	13	450	19.4	724	14	CB952493 AGENCOURT
	14	444.4	19.2	481	14	CB158774 K-EST0218
c	15	442	19.1	583	9	AI694348 wd45g04.x
c	16	437.8	18.9	462	13	BX109306 BX109306
c	17	435.8	18.8	439	9	AA633698 ag87a11.s
	18	431.6	18.6	899	12	BI246549 602958449
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c	20	422	18.2	422	9	AI580389 tm42f08.x
c	21	417	18.0	1055	9	AI654867 wb65c12.x
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c	23	410.2	17.7	478	9	AI015041 ov51a05.s
	24	406.4	17.5	901	12	BI827790 603075472
	25	404.8	17.4	1021	14	CK231266 ILLUMIGEN
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	27	396.4	17.1	721	12	BG972539 602841125
c	28	393.4	17.0	470	9	AA974327 oq10g06.s
	29	389	16.8	531	28	AQ386013 RPCI11-14
c	30	388.6	16.8	449	9	AI217703 qh15e09.x
	31	387.8	16.7	738	14	CB954127 AGENCOURT
	32	386.6	16.7	751	28	AQ748070 HS_5538_A
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c	37	376.8	16.2	566	14	CB433850 610302 MA
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	44	361.6	15.6	1193	12	BI102573 602889579
c	45	357	15.4	363	14	Z39483 HSC1BC022 n

## ALIGNMENTS

RESULT 1  
AY404343  
LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003  
DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY404343  
VERSION AY404343.1 GI:39760320  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1182)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1182)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
gene <1. .>1182  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517  
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Qy 518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 577  
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Qy	578	GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTG	637
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Qy	638	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	697
Db	181	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	240
Qy	698	TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTACA	757
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Db	301	GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC	360
Qy	818	TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC	877
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Qy	878	TTGATGGAAAAACCTATTAACCAGTACCACAAGACTTGGAGAACCTTCATTGCCAAGTTT	937
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Qy	998	GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG	1057
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Qy	1118	TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGC	1177
Db	661	TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGC	720
Qy	1178	GGGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC	1237
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Qy	1238	TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATT	1297
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Qy	1298	CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC	1357
Db	841	CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC	900
Qy	1358	AAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGC	1417
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Qy	1418	CCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCAC	1477



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Qy      1538 TTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCT 1597
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Qy      1598 GTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639
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# RESULT 2

AK050128

LOCUS AK050128 2197 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730018P11 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK050128

VERSION AK050128.1 GI:26340835

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2197)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .2197

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/mol\_type="mRNA"

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Db     152 TCTCTTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT 211

Qy     181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Qy	1198	GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA	1257
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Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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<http://image.llnl.gov>  
 Plate: LLAM13284 row: 1 column: 23  
 High quality sequence start: 17  
 High quality sequence stop: 671.

FEATURES  
 source Location/Qualifiers  
 1. .879  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6043558"  
 /tissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_92"  
 /note="Organ: testis; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 36.8%; Score 853.2; DB 13; Length 879;  
 Best Local Similarity 99.0%; Pred. No. 1.8e-231;  
 Matches 869; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 780 CTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTG 839  
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 Db 1 CTCATCTTCTACTGAAAGCAGAGATGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTG 60

Qy 840 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC 899  
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 Db 61 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC 120

Qy 900 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 959  
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 Db 121 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 180

Qy 960 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACA 1019  
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 Db 181 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACA 240

Qy 1020 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA 1079  
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 Db 241 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA 300

Qy 1080 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 1139  
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 Db 301 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 360

Qy 1140 TGGCTCACCCAAGCATCCGTCTGTTTGTGACCCACGGCGGGCAGAATAGCATAATGGAGG 1199  
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 Db 361 TGGCTCACCCAAGCATCCGTCTGTTTGTGACCCACGGCGGGCAGAATAGCATAATGGAGG 420



Qy 1200 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 1259  
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 Db 421 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 480  
 Qy 1260 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAG 1319  
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 Db 481 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAG 540  
 Qy 1320 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 1379  
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 Db 541 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 600  
 Qy 1380 TGGCTGCCAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 1439  
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 Db 601 TGGCTGCCAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 660  
 Qy 1440 GGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 1499  
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 Db 661 GGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 720  
 Qy 1500 AGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 1559  
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 Db 721 AGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 780  
 Qy 1560 GGA CTCTATGGCTTTGT-GGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCC 1618  
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 Db 781 GGA CTCTATGGCTTTGTGGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCTTGGGGCC 840  
 Qy 1619 AGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656  
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 Db 841 ACAAAGGGAAGGAGACCTAAAGCCAGGTGCACCCTTG 878

# RESULT 5

CD050395

LOCUS CD050395 916 bp mRNA linear EST 09-MAY-2003

DEFINITION AGENCOURT\_13977999 NIH\_MGC\_173 Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CD050395

VERSION CD050395.1 GI:30487290

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 916)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jamie Thompson, University of WI

cDNA Library Preparation: Gina Zastrow-Hayes

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: NDKM37 row: m column: 04  
High quality sequence start: 12  
High quality sequence stop: 721.

FEATURES  
source Location/Qualifiers  
1. .916  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic trophoblasts, made from WA01 stem cells"  
/lab\_host="DH10B TonA"  
/clone\_lib="NIH\_MGC\_173"  
/note="Vector: pDONR201; Site\_1: attP2; Site\_2: attP1;  
LIBR\_PRIMING - oligo dT; METHOD - full-length enriched;  
LIBR\_PROVIDER - Bradfield"

ORIGIN

Query Match 31.8%; Score 738; DB 14; Length 916;  
Best Local Similarity 95.0%; Pred. No. 1.4e-198;  
Matches 795; Conservative 0; Mismatches 36; Indels 6; Gaps 3;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	54	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	113
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	114	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	173
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	174	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	233
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	234	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	293
Qy	241	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	294	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	353
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	354	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	413
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	414	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	473
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	474	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	533
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	534	CTTCGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	592

Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600  
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 Db 593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 652  
 Qy 601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 660  
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 Db 653 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 712  
 Qy 661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720  
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 Db 713 GGGCCGAGTGAAGAATTTTCTGATNGTCTTTAGTTTCTGCAGGAAGCAACAGCACATGCA 772  
 Qy 721 GTCTACATTTGACAACACCATCAAGGAACA--TTTCACAGAAGGCTCTAGGCCAGTTTTG 778  
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 Db 773 GTCTACATTTGACAACACCATCCAAGGACATTTTTCACAGAGGGCTCTAGGGCCAGTTTT 832  
 Qy 779 TCTC---ATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTT 832  
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 Db 833 GTCCTCAATCTTCTACTGAAAAGCAAAAGTTGGTGGGTTTCAATTAACCTCTGGACTT 889

# RESULT 6

AY404345

LOCUS AY404345 1185 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404345

VERSION AY404345.1 GI:39760322

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .1185

/organism="Mus musculus"

/mol\_type="genomic DNA"

gene /db\_xref="taxon:10090"  
<1..>1185  
/locus\_tag="HCM1859"  
ORIGIN

Query Match 31.6%; Score 733.8; DB 29; Length 1185;  
Best Local Similarity 76.8%; Pred. No. 2.4e-197;  
Matches 910; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

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Qy      458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517
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Db       1 ATGGACTTCTTAAAAAATGAGAACTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGT 60

Qy      518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 577
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Db      61 TCTTTGCTAATTGTTGAAAAGCTTGGGAAACGATTTGTGTCCTTTCTCCCTTTCAATTT 120

Qy      578 GGCTCTTTGGAATTTGGGCTACCAA---TCCCCTTGTCTTATGTTCCAGTATCCGTTCC 634
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Db     121 AGCTATATGGACTTTGGGTTACCAAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCT 180

Qy      635 TTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGT 694
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Db     181 GGTCTAACTGACCAAATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTGAT 240

Qy      695 TTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTT 754
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Db     241 TTCTCCATGAAGCAAAGGGAAATCCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTT 300

Qy      755 ACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATT 814
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Db     301 GTGGAAGGCTCTCAGCCAGTGTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTC 360

Qy      815 AACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGA 874
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Db     361 AACTCTGACTTTGCTTTGGATTTTGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGA 420

Qy      875 GGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAG 934
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Db     421 GGTTTACTGGACAAACCTGTTTACGCCAATACCCCAAGACTTGGAGAATTTTATCTCTCAG 480

Qy      935 TTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAAT 994
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Db     481 TTTGGAGACTCAGGTTTTGTCTTGTGGCCCTGGGCTCTATAGTGAGCATGATTCAGTCC 540

Qy      995 CCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCAAGGGGTGATATGG 1054
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Db     541 AAGGAAATTATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGG 600

Qy     1055 AAGTGTCAAGTGTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGTG 1114
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Db     601 ACATGTAAGACTTCTCATTTGGCCCAAAGATGTCAAGTTTGGCCCAAATGTCAAAATCATG 660

Qy     1115 GACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCAC 1174
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Db     661 GATTGGCTTCACAGACTGACCTTCTAGCTCACCTAGCATTGCTGTTTGTCACTCAT 720
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Qy 1175 GCGGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCT 1234  
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 Db 721 GGAGGGATGAACAGTGTGATGGAGGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCA 780  
 Qy 1235 CTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCT 1294  
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 Db 781 TTTTTTTTTGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCT 840  
 Qy 1295 ATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAA 1354  
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 Db 841 ATTCAGCTACAGACGCTCAAGGCAGAGTCATTTGCGCTCACCATGAAAAAATCATAGAA 900  
 Qy 1355 GACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTC 1414  
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 Db 901 GACAAGAGGTACAAGTCTGCAGCAATGGCCTCCAAGATTATCAGGCACTCCCACCCACTG 960  
 Qy 1415 AGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACG 1474  
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 Db 961 ACCCCTGCCAGAGGCTTTTGGGCTGGATAGATCATATCTTGACAGACAGGGGGTGCAGCA 1020  
 Qy 1475 CACCTCAAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTT 1534  
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 Db 1021 CATCTCAAGCCATATGCTTTCCAGCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTC 1080  
 Qy 1535 GTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATG 1594  
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 Db 1081 CTCTTTCTCCTAGGGCTCATGCTGGGTACTTTGTGGCTTAGTGTAAGGTTCTTGTTGCT 1140  
 Qy 1595 GCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639  
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 Db 1141 GTAACCAGGTATCTGAGTATAGCAACGAAGGTCAAGGAGGCATAA 1185

# RESULT 7

AK041045

LOCUS AK041045 1353 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530069C13 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK041045

VERSION AK041045.1 GI:26334156

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.



Qy	361	AGAAACTTTAGGTGGCAGAGGAAAAATTTGAAAACCTATTATAAATGTTCTAGATACTTGGC	420
Db	373	AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG	432
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	433	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA	492
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	493	CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT	552
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC	600
Db	553	TGGGAAACGATTTGTGTCCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC	612
Qy	601	AA---TCCCCCTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTT	657
Db	613	AAGCGCCCCCTGTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT	672
Qy	658	CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT	717
Db	673	CTGGGGCCGAGTGAAGAACTTTCTGATGTTCTTTGATTTCTCCATGAAGCAAAGGAAAT	732
Qy	718	GCAGTCTACATTTGACAACACCATCAAGGAACATTCACAGAAGGCTCTAGGCCAGTTTT	777
Db	733	CCTTTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT	792
Qy	778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT	837
Db	793	GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT	852
Qy	838	TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA	897
Db	853	TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGG-TTACTGGACAAACCTGTTCA	911
Qy	898	ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCT	957
Db	912	GCCAATACCCCAAGACTTGGAGAATTTTATCTCTCAGTTTGGAGACTCAGGTTTTGTCCT	971
Qy	958	TGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAA	1017
Db	972	TGTGGCCCTGGGCTCTATAGTGAGCATGATTCAAGTCCAAGGAAATTATTAAGGAGATGAA	1031
Qy	1018	CAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCC	1077
Db	1032	CAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTTCTCATTGGCC	1091
Qy	1078	CAAAGATGTCCACCTGGCTGCAATGTGAAAATTTGTGGACTGGCTTCCTCAGAGTGACCT	1137
Db	1092	CAAAGATGTGAGTTTGGCCCCAATGTCAAAATCATGGATTGGCTTCACAGACTGACCT	1151
Qy	1138	CCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGA	1197
Db	1152	TCTAGCTCACCTAGCATTCTGTTTGTCACTCATGGAGGGATGAACAGTGTGATGGA	1211
Qy	1198	GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA	1257



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      ||| |||| ||||| || ||||| ||||| || | ||| ||||| |||||
Db      1212 GGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCATTTTTTTTTTGACCAACCTGAAAA 1271

Qy      1258 CATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGC 1317
      ||||| ||||| ||||| || || || ||||| ||||| || || || |||||
Db      1272 CATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCTATTTCAGCTACAGACGCTCAAGGC 1331

Qy      1318 AGAGACATTGGCTCTTAAGATG 1339
      |||| |||| || || | |||
Db      1332 AGAGTCATTTGCGCTCACCATG 1353

```

# RESULT 8

BI102968

LOCUS BI102968 978 bp mRNA linear EST 26-JUN-2001

DEFINITION 60288578F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5043978  
5', mRNA sequence.

ACCESSION BI102968

VERSION BI102968.1 GI:14553861

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 978)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11120 row: k column: 19

High quality sequence stop: 812.

## FEATURES

source

Location/Qualifiers

1. .978

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5043978"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI\_CGAP\_Kid14"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library. |"

## ORIGIN

Query Match 22.5%; Score 522.4; DB 12; Length 978;

Best Local Similarity 77.7%; Pred. No. 4.7e-137;

Matches 682; Conservative 0; Mismatches 191; Indels 5; Gaps 4;

Qy	644	GATCATGATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGG	703
Db	1	GACCAAATGGACTTTTGGGGCCGAGTGAAGAACATTCTGATGTTCTTTTCATTTACCAAG	60
Qy	704	AGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGC	763
Db	61	AAGCGAAGGGACATCTTTTCTCAATATGGCAATACTGTCCAGGAGCATTTTGC GGAAGGC	120
Qy	764	TCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGAC	823
Db	121	TCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGAC	180
Qy	824	TTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATG	883
Db	181	TTTGCCTTGGATTTTGTCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTG	240
Qy	884	GAAAAACCTATTAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGAC	943
Db	241	GACAAACCTGTTTCAGCCAATACCCCAAGACTTGGAGGATTTTATCTCTCAGTTTGGAGAC	300
Qy	944	TCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATC	1003
Db	301	TCAGGTTTTGTCTTGTGGCCCTGGACTCTGTAGTGAGCATGATTCAGTCCAAGGAAATT	360
Qy	1004	TTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAC	1063
Db	361	ATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG	420
Qy	1064	TGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT	1123
Db	421	AGTTCTCATTTGGCCCAAAGATGTGAGTTTGGCCCAAATGTCAAATCATGGATTGGCTT	480
Qy	1124	CCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAG	1183
Db	481	CCACAGATTGACCTTCTAGCTCACCTAGCATTCTGTTTGTACCCATGGGGGGATG	540
Qy	1184	AATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGA	1243
Db	541	AACAGTGTAAATGGAGGCTGTCCATCATGGAGTACCAATGGTAGGGATTCCATTTTTTGA	600
Qy	1244	GACCAGCCTGAAAACATGGTCCGAGTAGAAGCAAAAAGTTTGGTGTCTTCTATTAGTTA	1303
Db	601	GACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCTATTAGCTA	660
Qy	1304	AAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGA	1363
Db	661	CAGACACTCAAGGCAGAGTCATTTTGGCTCACCATGAAAGAAGTCATAGAAGACCAGAGG	720
Qy	1364	TACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACA	1423
Db	721	TACAAGACTGCAGCA-TGGCCTCCAAGGTTATCAGGAACCTCCACC--AATGACCTGGC	777
Qy	1424	CAGCGGCTGGTGGGCTGGATTGACCACGTC-CTCCAGACAGGGGGCGCGACGCACCTCAA	1482
Db	778	CAGAGGCTTGTGGGCTGGATTGATCACATCTTTGCAGACAGGGGGTGCAGCCCATCTCAA	837

Qy 1483 GCCCTATGTCTT-TCAGCAGCCCTGGCATGAGCAGTAC 1519  
 | |||| | | |||| | |||| | ||||  
 Db 838 AGCATATGGCTTCCCAGCAGGCTTGGCATAACGAGTAC 875

RESULT 9

BI559553

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001

DEFINITION 603252894F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5295502 5', mRNA sequence.

ACCESSION BI559553

VERSION BI559553.1 GI:15446867

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11747 row: k column: 23

High quality sequence stop: 726.

FEATURES

source

Location/Qualifiers

1. .761

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5295502"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_97"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.2 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is

a NIH\_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 12; Length 761;

Best Local Similarity 80.7%; Pred. No. 1.9e-127;

Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;



IMAGE:2663780 3' similar to SW:CGT\_RAT Q09426  
 2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,  
 mRNA sequence.

ACCESSION AW173071  
 VERSION AW173071.1 GI:6439019  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 694)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 412.

FEATURES  
 source Location/Qualifiers  
 1. .694  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2663780"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NbHL19W, testis NHT, and B-cell  
 NCI\_CGAP\_GCB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo. "

#### ORIGIN

Query Match 20.0%; Score 463.6; DB 10; Length 694;  
 Best Local Similarity 83.5%; Pred. No. 2.4e-120;  
 Matches 537; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 268 TAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGACCTGAAGATCATCAAAG 327  
 || |||| | ||| || || |||| | || | |||||  
 Db 643 TATAAAGAGAAGCAAAATTCATACAGGTATCCGGGTGGTTTTTCACCTAAGATCATCAAAA 584

QY 328 AGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATT 387  
 |||| |||| ||| ||||| || | ||| | ||| | ||||| | |||  
 Db 583 AGAA-TTAAGAAGCATTTTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATC 525

QY 388 TGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAG 447  
 |||| | | || | | ||| || | | || || || |||| ||| ||









REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1723)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .1723  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM\_DB:D630011D02"  
 /db\_xref="MGI:2422342"  
 /db\_xref="taxon:10090"  
 /clone="D630011D02"  
 /tissue\_type="kidney"  
 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="0 day neonate"

misc\_feature 1. .1723  
 /note="hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 11; Length 1723;  
 Best Local Similarity 69.1%; Pred. No. 4.9e-117;  
 Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTTAGA	60
Db	41	AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTCAAGGGCTCCACATAT	100
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCCT	120
Db	101	TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCTTTTCTTGAGGTTAT	160
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	161	TCTCTTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	220
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	221	GATAAGCCGTGTGTCGCAAGTTCCTCATGAAGGTGGCCACAATGTGACCAAACCTCTTTA	280
Qy	241	CAAAAGAGGTCTTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	281	TGAAA---GTGCTAATATCCCAGATTTTAGAAAGGAAAACCATCATATCAAGTTATTAA	337
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	338	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA	397
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	398	AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG	457
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA	480
Db	458	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA	517
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	518	CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT	577
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCACCTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	578	TGGGAAACGATTTGTGTCCTTCTTCCCTTTCATTTAGCTATATGGACTTTGGGTTACC	637
Qy	601	AA---TCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTT	657
Db	638	AAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTCTGGTCTAACTGACCAAATGGACTT	697
Qy	658	CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT	717
Db	698	CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTGATTCTCCATGAAGCAAAGGGAAAT	757
Qy	718	GCAGTCTACATTTGACAACACCATCAAGGAACATTCACAGAAGGCTCTAGGCCAGTTTT	777
Db	758	CCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT	817
Qy	778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT	837
Db	818	GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTGTCAACTCTGACTTTGCTTTGGATTT	877
Qy	838	TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA	897

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      ||||| || ||| ||||| || ||||| ||||| || ||| ||||| || |
Db      878 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA 937

Qy      898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTT 936
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Db      938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

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RESULT 13

CB952493

LOCUS CB952493 724 bp mRNA linear EST 29-APR-2003

DEFINITION AGENCOURT\_13692869 NIH\_MGC\_176 Mus musculus cDNA clone  
IMAGE:30303573 5', mRNA sequence.

ACCESSION CB952493

VERSION CB952493.1 GI:30208612

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 724)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Michael Brownstein Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM74 row: e column: 22

High quality sequence stop: 541.

FEATURES

source

Location/Qualifiers

1. .724

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:30303573"

/lab\_host="DH10B (T1-phage-resistant)"

/clone\_lib="NIH\_MGC\_176"

/note="Organ: kidney; Vector: pDNR-LIB; Site\_1: SfiI  
(ggcattatggcc); Site\_2: SfiI (ggccgcctcgcc); cDNA made  
by oligo-dT priming and directionally cloned. 5' and 3'  
adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and

5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.5 kb  
size fraction. Library created in the laboratory of M.

Brownstein (NIMH, NIH). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 19.4%; Score 450; DB 14; Length 724;  
Best Local Similarity 78.3%; Pred. No. 1.9e-116;

Matches 565; Conservative 0; Mismatches 155; Indels 2; Gaps 2;

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Qy      685 GTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA 744
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Db      3 GTTCCTTGATTTCTCCATGAAGCAAAGGGAAATCCTTTCTCAGTATGACAGCACTATCCA 62

Qy      745 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTT 804
      ||| |||| | |||| || | |||| |||| | |||| |||| || || ||
Db      63 GGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCT 122

Qy      805 GTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGT 864
      |||| | |||| |||| || || |||| || || || |||| || || ||
Db      123 GTGGTTTGTCAACTCTGACTTTGCTTTGGATTTTGTCTCGTCCCCTGTTTCCCAACACAGT 182

Qy      865 TTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTT 924
      |||| |||| || || || |||| || | || || || |||| || || ||
Db      183 CTATGTGGGAGGTTTACTGGACAAACCTGTTTCAGCCAATACCCCAAGACTTGGAGAATTT 242

Qy      925 CATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACAC 984
      || | |||| || || || |||| || || || || || || || || ||
Db      243 TATCTCTCAGTTTGGGAGACTCAGGTTTTGTCTTGTGGCCCTGGGCTCTATAGTGAGCAT 302

Qy      985 CTGTCAGAATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGG 1044
      |||| |||| | |||| |||| || || || || || || || || || ||
Db      303 GATTCAGTCCAAGGAAATTATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGG 362

Qy      1045 GGTGATATGGAAGTGTCTAGTGTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAATGT 1104
      |||| |||| || || || |||| |||| |||| || || || || || ||
Db      363 GGTGCTATGGACATGTAAGACTTCTCATTGGCCCCAAGATGTCTAGTTTGGCCCCAAGT 422

Qy      1105 GAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTT 1164
      |||| |||| |||| || || |||| || || |||| || || || || ||
Db      423 CAAAATCATGGATTGGCTTCCACAGACTGACCTTCTAGCTCACCTAGCATTCGTCTGTT 482

Qy      1165 TGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGT 1224
      |||| || || || || || || || || || || || || || || || ||
Db      483 TGTCACTCATGGAGGGATGAACAGTGTGATGGAGGCTGTCCATCATGGAGTACCCATGGT 542

Qy      1225 GGGGA-TCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 1283
      |||| || | | || || || || |||| |||| |||| |||| || || ||
Db      543 GGGGATTCCATTTTTTTTTTTGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACC 602

Qy      1284 TTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAC 1343
      |||| |||| || || || || || || || || || || || || || ||
Db      603 TTGGTGTTCATTTCAGCTACAGACGCCTCAGGCAGAGTCATTTGCGCTCACCATGAAAA 662

Qy      1344 AAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTATCCTGCGCT 1403
      |||| | |||| || || |||| || || || || || || || || || ||
Db      663 AAATCCTAGAAGAC-AGAGGTACAAGTCTGCAGCAATGGCCTCCAAGATTATCAGGCAC 721

Qy      1404 CC 1405
      ||
Db      722 CC 723

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LOCUS CB158774 481 bp mRNA linear EST 29-JAN-2003  
 DEFINITION K-EST0218183 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-14-D07  
 5', mRNA sequence.  
 ACCESSION CB158774  
 VERSION CB158774.1 GI:28143912  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 481)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 14 row: D column: 07  
 High quality sequence stop: 481.  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="L18POOL1n1-14-D07"  
 /cell\_line="SNU-354+Cho-CK+Choi-CK+HLK-3"  
 /lab\_host="Top10F"  
 /clone\_lib="L18POOL1n1"  
 /note="Organ: Liver; Vector: pT7T3-Pac; Site\_1: EcoRI;  
 Site\_2: NotI; The library was contributed by the Soares  
 laboratory and it was constructed as described by Bonaldo,  
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
 6(9): 791-806. RNA was prepared from harvested cell  
 culture."  
 ORIGIN  
 Query Match 19.2%; Score 444.4; DB 14; Length 481;  
 Best Local Similarity 99.8%; Pred. No. 6.3e-115;  
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 Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60  
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 Db 36 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 95  
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 Db 96 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 155  
 Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
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 Db 156 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGATGCCATTATCTACT 215

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240  
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 Db 276 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 335  
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 Db 456 GTTGCAGTGCAGTCATTTTTTAAATA 481

# RESULT 15

AI694348/c

LOCUS AI694348 583 bp mRNA linear EST 17-DEC-1999

DEFINITION wd45g04.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:2331126 3' similar to SW:CGT\_MOUSE Q64676  
 2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,  
 mRNA sequence.

ACCESSION AI694348

VERSION AI694348.1 GI:4971688

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Insert Length: 929 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 462.

FEATURES Location/Qualifiers

source 1. .583

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2331126"

/lab\_host="DH10B"

/clone\_lib="Soares\_NFL\_T\_GBC\_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI\_CGAP\_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Query Match 19.1%; Score 442; DB 9; Length 583;  
Best Local Similarity 85.0%; Pred. No. 3.3e-114;  
Matches 493; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Search completed: May 16, 2004, 14:01:53  
Job time : 8801 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 04:18:54 ; Search time 14319 Seconds  
(without alignments)  
7022.546 Million cell updates/sec

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Sequence: 1 aggggtcccttagccggg'gcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
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11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
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41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	2	2320	100.0	2320	9	AY358416	AY358416 Homo sapi	
	3	2310.2	99.6	2341	6	AX136141	AX136141 Sequence	
	4	2310.2	99.6	2341	6	BD123523	BD123523 Secretory	
	5	2310.2	99.6	2341	9	AK075383	AK075383 Homo sapi	
	6	2102.8	90.6	2944	6	AX548037	AX548037 Sequence	
	7	1281.6	55.2	2082	6	AX359921	AX359921 Sequence	
	8	1281.6	55.2	2797	6	AX155211	AX155211 Sequence	
	9	1281.6	55.2	2823	6	AX714604	AX714604 Sequence	
	10	1281.6	55.2	2823	9	AK057066	AK057066 Homo sapi	
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	12	1212	52.2	1572	6	AX359923	AX359923 Sequence	
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	14	957.6	41.3	179513	9	AC016612	AC016612 Homo sapi	
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	16	912.4	39.3	2210	10	AK128903	AK128903 Mus muscu	
	17	912.2	39.3	2192	10	BC034837	BC034837 Mus muscu	
	18	912.2	39.3	2196	10	BC022134	BC022134 Mus muscu	
	19	910.8	39.3	2212	6	AX155214	AX155214 Sequence	
	20	909.2	39.2	2228	10	BC025940	BC025940 Mus muscu	
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	22	595.4	25.7	148069	2	AC025476	AC025476 Homo sapi	
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	25	593.4	25.6	1842	6	AX747286	AX747286 Sequence	
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	28	575.4	24.8	5002	9	AK125803	AK125803 Homo sapi	
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	30	573.4	24.7	3108	9	BC035012	BC035012 Homo sapi	
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c	32	538.4	23.2	594	6	AX136632	AX136632 Sequence	
c	33	538.4	23.2	594	6	BD123872	BD123872 Secretory	

	34	444.8	19.2	88948	2	AC008947	AC008947 Homo sapi
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	37	308.2	13.3	251769	2	AC117913	AC117913 Rattus no
	38	308	13.3	156499	2	AC132893	AC132893 Mus muscu
c	39	245.2	10.6	211178	10	AC139209	AC139209 Mus muscu
c	40	239.2	10.3	125145	2	AC022136	AC022136 Homo sapi
c	41	239.2	10.3	165304	9	AC112204	AC112204 Homo sapi
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	43	167.2	7.2	3598	10	AK128994	AK128994 Mus muscu
	44	167.2	7.2	4185	10	RNU07683	U07683 Rattus norv
	45	165.6	7.1	2633	10	RATCERUDPG	L21698 Rat ceramid

# ALIGNMENTS

## RESULT 1

AX697213

LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 281 from Patent WO0078961.

ACCESSION AX697213

VERSION AX697213.1 GI:29498151

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,  
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,  
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same

JOURNAL Patent: WO 0078961-A 281 28-DEC-2000;  
Genentech Inc. (US)

FEATURES Location/Qualifiers  
source 1. .2320  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180

Db	121		GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
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Qy	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Qy	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
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Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
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Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
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Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
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Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860

Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920  
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Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
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## RESULT 2

AY358416

LOCUS AY358416 2320 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA, complete cds.

ACCESSION AY358416

VERSION AY358416.1 GI:37181956

KEYWORDS FLI\_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2320)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale

Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 2320)  
AUTHORS Clark, H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Query Match 100.0%; Score 2320; DB 9; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
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Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
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Db	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
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Db	301		TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361		AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Qy	481		CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481		CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
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Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
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Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
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Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAATTTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140



Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
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# RESULT 3

AX136141

LOCUS AX136141 2341 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 63 from Patent EP1067182.

ACCESSION AX136141

VERSION AX136141.1 GI:14272549

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 63 10-JAN-2001;  
 Helix Research Institute (JP)

FEATURES

source

Location/Qualifiers

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CDS

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ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	87	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	146
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
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Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
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Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
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Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
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 LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Secretory protein or membrane protein.  
 ACCESSION BD123523  
 VERSION BD123523.1 GI:23218468  
 KEYWORDS JP 2002017376-A/32.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2341)  
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.  
 TITLE Secretory protein or membrane protein  
 JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002017376-A/32  
 PD 22-JAN-2002  
 PF 07-JUL-2000 JP 2000253173  
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 PI SUGIYAMA,  
 PI KOJI HAYASHI  
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ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;  
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
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Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
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Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
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RESULT 5

AK075383

LOCUS AK075383 2341 bp mRNA linear PRI 03-SEP-2002  
 DEFINITION Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar  
 to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).

ACCESSION AK075383

VERSION AK075383.1 GI:22761433

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,  
 Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,  
 Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2341)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass  
 sequencing, clone selection and full insert sequencing: Helix  
 Research Institute (supported by Japan Key Technology Center etc.);  
 cDNA library construction: Institute of Medical Science, University  
 of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES Location/Qualifiers

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# ORIGIN

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Query Match      99.6%; Score 2310.2; DB 9; Length 2341;
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Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	1527	GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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# RESULT 6

AX548037

LOCUS AX548037 2944 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 13 from Patent WO02066654.

ACCESSION AX548037

VERSION AX548037.1 GI:25813133

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,  
 Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,  
 Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,  
 Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 02066654-A 13 29-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .2944

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Best Local Similarity 95.5%; Pred. No. 0;

Matches 2216; Conservative 0; Mismatches 2; Indels 102; Gaps 1;

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RESULT 7

AX359921

LOCUS AX359921 2082 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 1 from Patent WO0202774.

ACCESSION AX359921

VERSION AX359921.1 GI:18675563

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby,K.R., Cook,W.J. and Spaltmann,F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 1 10-JAN-2002;  
Millennium Pharmaceuticals, Inc. (US)

FEATURES Location/Qualifiers

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CDS 145. .1716



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# ORIGIN

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Query Match          55.2%;  Score 1281.6;  DB 6;  Length 2082;
Best Local Similarity 85.9%;  Pred. No. 0;
Matches 1422;  Conservative 0;  Mismatches 234;  Indels 0;  Gaps 0;

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Qy 1267 AGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAGTTAAAGAAGCTCAAGGCAGAGACATT 1326  
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Qy 1327 GGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGC 1386  
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Query Match		55.2%;	Score 1281.6;	DB 6;	Length 2797;
Best Local Similarity		85.9%;	Pred. No. 0;		
Matches 1422;		Conservative	0;	Mismatches 234;	Indels 0; Gaps 0;
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Qy	67	CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTC	126		
Db	118	CATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTC	177		
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Qy	187	CCGGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG	246		
Db	238	CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG	297		
Qy	247	AGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCT	306		
Db	298	AAAGTTTTTGTATCCAGATATTAAAGAGGAGGAAAAATCATACCAAGTTATCAGGTGGTT	357		
Qy	307	TGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAC	366		
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Qy	367	TTTAGGTGGCAGAGGAAAAATTTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCA	426		
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Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTT	1026
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## RESULT 9

AX714604

LOCUS            AX714604                            2823 bp        DNA        linear        PAT 15-APR-2003

DEFINITION Sequence 1288 from Patent EP1293569.

ACCESSION AX714604

VERSION AX714604.1 GI:29889557

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.

TITLE Full-length cDNAs

JOURNAL Patent: EP 1293569-A 1288 19-MAR-2003;  
Helix Research Institute (JP) ; Research Association for  
Biotechnology (JP)

FEATURES Location/Qualifiers

source

1. 2823

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## ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2823;

Best Local Similarity 85.9%; Pred. No. 0;

Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG 66  
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QY           67 CATGGCTGGGCAGCGAGTGCTTCTTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTC   126  
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Db 157 CATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTC 216

QY           127 AGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA         186  
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Db 217 AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA 276

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Qy 247 AGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCT 306  
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Db	397	TTCACCTGAAGATCATCAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGC	456
Qy	367	TTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCA	426
Db	457	ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA	516
Qy	427	GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGA	486
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Qy	487	CATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAA	546
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Qy	547	GCCATTTGTGGCCATTCTTTCCACTTCATTCCGCTCTTTGGAATTTGGGCTACCAATCCC	606
Db	637	ACCATTTGTGGCCATTCTTCCCACCACATTCCGCTCTTTGGATTTTGGGCTACCAAGCCC	696
Qy	607	CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	666
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Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCT	786
Db	817	ATTTGACAACACCATCAAGGAGCATTTCCCAGAAGGCTCTAGGCCAGTTTGTCTCATCT	876
Qy	787	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACC	846
Db	877	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGATTTTGCCTTTGATTTTGCCCGGCC	936
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Qy	907	ACAAGACTTGGGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCCCTTGTGACCTT	966
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Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAATGCCTT	1026
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JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2823)  
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

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# ORIGIN

Query Match 55.2%; Score 1281.6; DB 9; Length 2823;  
Best Local Similarity 85.9%; Pred. No. 0;  
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AX327327

DEFINITION Sequence 12 from Patent WO0179468.

VERSION AX327327.1 GI:18097873

SOURCE	Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

AUTHORS Policky, J.L., Hafalia, A., Burford, N., Ring, H.Z., Lal, P.,

Tribouley,C.M., Yao,M.G., Yue,H., Tang,Y.T., Patterson,C., Das,D., Sanjanwala,M.S., Gandhi,A.R., Reddy,R., Khan,F.A., Baughn,M.R., Ramkumar,J., Griffin,J.A. and Au-Young,J.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 0179468-A 12 25-OCT-2001;  
Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers  
source 1. .2086  
/organism="Homo sapiens"  
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ORIGIN

Query Match 55.2%; Score 1280; DB 6; Length 2086;  
Best Local Similarity 85.8%; Pred. No. 0;  
Matches 1421; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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AC008947/c

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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 88948)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Sequencing of Human Chromosome 5  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 88948)  
 AUTHORS DOE Joint Genome Institute.



TITLE Direct Submission  
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On May 5, 2000 this sequence version replaced gi:6997051.  
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 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>  
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 Project Information  
 Center Project Name: 754542  
 Center clone name: CITB-H1\_2330L9  
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 Summary Statistics  
 Consensus quality: 67454 bases at least Q40  
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 Estimated insert size: 85000; pulse field gel estimation  
 Estimated insert size: 87148; sum-of-contigs estimation  
 Quality coverage: 3.94 in Q20 bases; pulse field gel estimation  
 Quality coverage: 3.84 in Q20 bases; sum-of-contigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 19 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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*      75414      88948: contig of 13535 bp in length.

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FEATURES
    source          Location/Qualifiers
                    1. .88948
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /chromosome="5"
                    /clone="CTD-2330L9"
                    /clone_lib="CalTech human BAC library D"

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# ORIGIN

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Query Match          41.3%;  Score 957.6;  DB 2;  Length 88948;
Best Local Similarity 99.6%;  Pred. No. 1.1e-242;
Matches 960;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

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Qy      1357 CAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG 1416
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4584 CAACAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG 4525

Qy      1417 CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA 1476
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4524 CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA 4465

Qy      1477 CCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTTGT 1536
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4464 CCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTTGT 4405

Qy      1537 GTTCTGCTGGGGCTCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC 1596
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4404 GTTCTGCTGGGGCTCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC 4345

Qy      1597 TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4344 TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 4285

Qy      1657 GCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCA 1716
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4284 GCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCA 4225

Qy      1717 GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC 1776
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4224 GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC 4165

Qy      1777 AAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT 1836
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4164 AAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT 4105

Qy      1837 GCTAGCAGAAATCTTTCCAGTCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATG 1896
        ||||||||| ||||||||||||||||||||||||||||||||||||||||||||

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Db	4104	GCTAGCAGAATTCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATG	4045
Qy	1897	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	1956
Db	4044	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	3985
Qy	1957	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	2016
Db	3984	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	3925
Qy	2017	GACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAA	2076
Db	3924	GACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAA	3865
Qy	2077	AGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	2136
Db	3864	AGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	3805
Qy	2137	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	2196
Db	3804	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	3745
Qy	2197	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	2256
Db	3744	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	3685
Qy	2257	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	2316
Db	3684	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	3625
Qy	2317	CTAA	2320
Db	3624	CTAA	3621

#### RESULT 14

AC016612

LOCUS AC016612 179513 bp DNA linear PRI 06-SEP-2001

DEFINITION Homo sapiens chromosome 5 clone CTD-2197M16, complete sequence.

ACCESSION AC016612

VERSION AC016612.6 GI:15451670

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission  
 JOURNAL Submitted (20-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 REFERENCE 4 (bases 1 to 179513)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Sep 6, 2001 this sequence version replaced gi:11908274.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov  
 Finishing Completed at Stanford Human Genome Center  
 www-shgc.stanford.edu  
 Quality: Phrap Quality >=40 99.4% of Sequence;  
 Estimated Total Number of Errors is 0.8.  
 STS Content:  
 SHGC-141485 G63682  
 SHGC-104791 G58536.

FEATURES Location/Qualifiers  
 source 1. .179513  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
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#### ORIGIN

Query Match 41.3%; Score 957.6; DB 9; Length 179513;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-242;  
 Matches 960; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1357	CAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG	1416
Db	48080	CAACAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG	48139
Qy	1417	CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA	1476
Db	48140	CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA	48199
Qy	1477	CCTCAAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGT	1536
Db	48200	CCTCAAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGT	48259
Qy	1537	GTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC	1596
Db	48260	GTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC	48319
Qy	1597	TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG	1656
Db	48320	TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG	48379
Qy	1657	GCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCA	1716
Db	48380	GCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCA	48439
Qy	1717	GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC	1776

Db	48440	GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC	48499
Qy	1777	AAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT	1836
Db	48500	AAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT	48559
Qy	1837	GCTAGCAGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATG	1896
Db	48560	GCTAGCAGAATTCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATG	48619
Qy	1897	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	1956
Db	48620	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	48679
Qy	1957	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	2016
Db	48680	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	48739
Qy	2017	GACCTAGTCAGCCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAA	2076
Db	48740	GACCTAGTCAGCCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAA	48799
Qy	2077	AGACACCTTGCAATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	2136
Db	48800	AGACACCTTGCAATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	48859
Qy	2137	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	2196
Db	48860	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	48919
Qy	2197	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	2256
Db	48920	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	48979
Qy	2257	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	2316
Db	48980	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	49039
Qy	2317	CTAA	2320
Db	49040	CTAA	49043

# RESULT 15

AX155213

LOCUS	AX155213	1569 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 3 from Patent WO0138505.				
ACCESSION	AX155213				
VERSION	AX155213.1 GI:14536692				
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Adler,D.A., Dong,D.L., Pownder,S., Gao,Z. and Conklin,D.C.				
TITLE	Secreted protein, zalpha37				
JOURNAL	Patent: WO 0138505-A 3 31-MAY-2001;				

ZymoGenetics, Inc. (US)  
 FEATURES Location/Qualifiers  
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             /note="Degenerate sequence"

ORIGIN

Query Match 40.7%; Score 944.8; DB 6; Length 1569;  
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 Matches 822; Conservative 343; Mismatches 403; Indels 0; Gaps 0;

Qy	68	ATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCTCA	127
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Db	1	ATGGTNGGNCARMGNGTNYTNYTNYTNGTNGCNTTYTNYTNWSNGGNGTNYTNYTNWSN	60
Qy	128	GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC	187
		:      :::     :::         :: :: :: :: :: :: :: :: :: :: ::	
Db	61	GARGCNGCNAARATHYTNACNATHWSNACNYTNGGNGGWSNCAYTAYYTNYTNYTNGAY	120
Qy	188	CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGA	247
		:    ::	
Db	121	MNGTGNWSNCARATHYTNCARGARCA YGGNCAYAA YGTNACNATGYTNCAYCARWSNGGN	180
Qy	248	GGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTT	307
		::        ::	
Db	181	AARTYYTNATHCCNGAYATHAARGARGARGARAARWSNTAYCARGTNATHMGNTGGTTY	240
Qy	308	GCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGAAGAACT	367
		:    ::	
Db	241	WSNCCNGARGAYCAYCARARMGNATHAARAARCA YTTYGAYWSNTAYATHGARACNGCN	300
Qy	368	TTAGGTGGCAGAGGAAAATTTGAAAAC TTATTAATGTTCTAGAATACTTGGCGTTGCAG	427
		:   ::	
Db	301	YTNGAYGGNMGNAARGARWSNGARGCNYTNGTNAARYTNATGGARATHTTYGGNACNCAR	360
Qy	428	TGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGAC	487
		::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
Db	361	TGYWSNTAYYTNYNWSNMGNAARGAYATHATGGAYWSNYTNAARAAYGARAAYTAYGAY	420
Qy	488	ATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAG	547
		:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
Db	421	YTNGTNTTYGTNGARGCNTTYGAYTTYTGYSNTTYTNYTATHGCGNARAARYTNGTNAAR	480
Qy	548	CCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCC	607
		:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
Db	481	CCNTTYGTNGCNATHYTNCNACNACNTTYGGNWSNYTNGAYTTYGGNYTNCNWSNCCN	540
Qy	608	TTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGA	667
		: ::	
Db	541	YTNWSNTAYGTNCCNGTNTTYCCNWSNYTNYTNACNGAYCAYATGGAYTTYTGGGGNMGN	600
Qy	668	GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA	727
		:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
Db	601	GTNAARAAYTTYTNYTATGTTYTYTWSNTTYWSNMGNWSNCARTGGGAYATGCARWSNACN	660

Qy 728 TTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTT 787  
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 Db 661 TTYGAYAAAYACNATHAARGARCAYYTTYCCNGARGGNWSNMGNCCNGTNYTNWSNCAYYTN 720

Qy 788 CTAAGTGAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTTGATTTTGCTCGACCT 847  
 :| :| |:|:| |:|:| | |:|:| | |:|:| |:|:| |:|:| |:|:| |:|:| :| | |  
 Db 721 YTNYTNAARGCNGARYTNTGGTTYGTNAAYWSNGAYTTYGCNTTYGAYTTYGCNMGNCCN 780

Qy 848 CTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA 907  
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 Db 781 YTNYTNCNAAYACNGTNTAYATHGGNGGNYTNATGGARAARCCNATHAARCCNGTNCN 840

Qy 908 CAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTG 967  
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 Db 841 CARGAYYTNGAYAAYYTYATHGCNAAYTTYGGNGAYGCNGGNTTYGTNYTNGTNGCNTTY 900

Qy 968 GGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT 1027  
 | | : : | | | | |:|:| : |:|:| : |:|:| : |:|:| |:|:| |:|:| | | :  
 Db 901 GGNWSNATGYTNAAYACNCAYCARWSNCARGARGTNYTNAAARATGCAYAAAYGCNTTY 960

Qy 1028 GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGATGTC 1087  
 | | |:|:| | | |:|:| | | |:|:| | | |:|:|:| : : |:|:| | | : | |:|:|  
 Db 961 GCNCAYYTNCNCARGGNGTNATHTGGACNTGYCARWSNWSNCAYTGGCCNMGNAYGTN 1020

Qy 1088 CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1147  
 |:|:| | | | |:|:| |:|:|:| |:|:|:| | | |:|:| |:|:| :| | | | :  
 Db 1021 CAYYTNGCNACNAAYGTNAARATHGTNGAYTGGYTNCNCARWSNGAYYTNYTNGCNACAY 1080

Qy 1148 CCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG 1207  
 | | : : |:|:| :| |:|:| | | |:|:| | | |:|:|:| : | |:|:| | | |:|:|  
 Db 1081 CCNWSNATHMGNYTNTTYGTNACNCAYGGNGGNCARAAYSNGTNGTNGGARGCNATHMGN 1140

Qy 1208 CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA 1267  
 |:|:| | | | | | | | | | :| |:|:|:| :| |:|:| | | :|  
 Db 1141 CAYGGNGTNCNATGGTNGGNYTNCCNGTNAAYGGNGAYCARCAYGGNAAYATGGTNMGN 1200

Qy 1268 GTAGAAGCCAAAAAGTTTGGTGTCTTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTG 1327  
 | | | | |:|:| | :| | | : : |:|:| : | | | | | | :|  
 Db 1201 GTNGTNGCNAAARAAAYTAYGGNGTNWSNATHMGNYTNAAYCARGTNACNGCNGAYACNYTN 1260

Qy 1328 GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC 1387  
 | :| | | |:|:| |:|:| | | |:|:| |:|:| |:|:|:| | | | | | | | |  
 Db 1261 ACNYTNACNATGAARCARGTNATHGARGAYAARMGNTAYAARWSNGCNGTNGTNGCNGCN 1320

Qy 1388 AGTGTGCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC 1447  
 : : | | |:|:| | : : | | | :| : : | | | |:|:| :| | | | |:|:|:|  
 Db 1321 WSGTNGATHYTNCAYWSNCARCCNYTNWSNCCNGCNCARMGNYTNGTNGGNTGGATHGAY 1380

Qy 1448 CACGTCTCTCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGG 1507  
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 Db 1381 CAYATHYTNCARACNGGNGGNCNACNCAYYTNAARCCNTAYGCNTTYCARCARCCNTGG 1440

Qy 1508 CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1567  
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 Db 1441 CAYGARCARTAYYTNAATHGAYGTNTTYGTNTTYTNYTNGGNYTNACNYTNGGNACNATG 1500

Qy 1568 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1627

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      |||:| ||:| | |::| :| || | | | | |||:| :| || || :| ||:|
Db      1501 TGGYTNTGYGGNAARYTNYTNGGNGTNGTNGCNMGNTGGYTNTMGNGGNGCNMGNAARGTN 1560
Qy      1628 AAGGAGAC 1635
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Db      1561 AARAARAC 1568

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Search completed: May 16, 2004, 11:35:04  
Job time : 14326 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:20:03 ; Search time 1303 Seconds  
(without alignments)  
7563.944 Million cell updates/sec

Title: US-10-017-867A-281  
Perfect score: 2320  
Sequence: 1 agggtccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
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2	2320	100.0	2320	3	AAA37101	Aaa37101 Human PRO
3	2320	100.0	2320	4	AAF54401	Aaf54401 Primer #8
4	2320	100.0	2320	8	ACD68440	Acd68440 Novel hum
5	2320	100.0	2320	8	ACH04542	Ach04542 Human cDN
6	2320	100.0	2320	8	ACD68086	Acd68086 Novel hum
7	2320	100.0	2320	9	ADC18150	Adc18150 Human PRO

	8	2320	100.0	2320	9	ADD70796	Add70796 Human cDN
	9	2320	100.0	2320	9	ADD39873	Add39873 Human cDN
	10	2320	100.0	2320	9	ADD70319	Add70319 Human cDN
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	12	2320	100.0	2320	9	ADD39396	Add39396 Human cDN
	13	2320	100.0	2320	9	ADD38919	Add38919 Human cDN
	14	2320	100.0	2320	9	ADD40350	Add40350 Human cDN
	15	2320	100.0	2320	9	ADE50571	Ade50571 Human cDN
	16	2320	100.0	2320	9	ADE20183	Ade20183 Human cDN
	17	2320	100.0	2320	9	ADE50094	Ade50094 Human cDN
	18	2320	100.0	2320	9	ADE21652	Ade21652 Human cDN
	19	2310.2	99.6	2341	5	AAF93775	Aaf93775 Human cDN
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	21	2063.4	88.9	2074	6	AAS62475	Aas62475 cDNA sequ
	22	1281.6	55.2	2797	4	AAD06821	Aad06821 Human sec
	23	1281.6	55.2	2823	7	ADA53720	Ada53720 Human cod
	24	1280	55.2	2086	6	AAD24667	Aad24667 Human dru
	25	1270.4	54.8	1851	6	ABK90831	Abk90831 cDNA enco
	26	1257.6	54.2	2082	6	AAD25345	Aad25345 Human UDP
	27	1212	52.2	1572	6	ABL57726	Abl57726 Human sbg
	28	1147.8	49.5	2268	8	ADA21188	Ada21188 Human sec
	29	1147.8	49.5	2426	7	ABX70800	Abx70800 Novel hum
	30	956.4	41.2	1182	6	ABL57725	Abl57725 Human sbg
	31	944.8	40.7	1569	4	AAD06822	Aad06822 Human sec
	32	910.8	39.3	2212	4	AAD06823	Aad06823 Mouse sec
c	33	808.8	34.9	2721	5	AAS84832	Aas84832 DNA encod
	34	789	34.0	1569	4	AAD06824	Aad06824 Mouse sec
c	35	708.2	30.5	1898	4	ABA09537	Aba09537 Human PRO
	36	595.2	25.7	770	5	AAF93971	Aaf93971 Primer sp
	37	593.4	25.6	1842	9	ADB62657	Adb62657 Human cDN
c	38	538.4	23.2	594	5	AAF94120	Aaf94120 Primer sp
	39	487.6	21.0	2220	5	AAS81804	Aas81804 DNA encod
	40	433.6	18.7	42999	6	ABK90832	Abk90832 Genomic D
c	41	399.6	17.2	659	5	AAS81803	Aas81803 DNA encod
	42	319.6	13.8	923	4	AAS41046	Aas41046 cDNA enco
	43	319.4	13.8	981	4	AAS41586	Aas41586 cDNA enco
	44	319.4	13.8	981	4	AAL01667	Aal01667 Human rep
	45	239.2	10.3	5973	4	AAL05664	Aal05664 Human rep

#### ALIGNMENTS

##### RESULT 1

AAC58107

ID AAC58107 standard; cDNA; 2320 BP.

XX

AC AAC58107;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human PRO1780 nucleotide sequence SEQ ID NO:12.

XX

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
KW identification; tumourigenesis; anticancer; detection; ss.

XX

OS Homo sapiens.

XX  
 PN WO200053750-A1.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-DEC-1999; 99WO-US028551.  
 XX  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028634.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2000-594320/56.  
 DR P-PSDB; AAB24025.  
 XX  
 PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
 PT the growth of tumors in mammals, and to identify inhibitors of PRO  
 PT polypeptide activity or expression.  
 XX  
 PS Claim 50; Fig 9; 226pp; English.  
 XX  
 CC The present invention describes an antibody that binds to a human protein  
 CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;  
 CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;  
 CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer  
 CC activity and can be used to diagnose tumours in mammals, by detecting  
 CC complex formation when the antibody is contacted with test cells.  
 CC Increased expression of genes encoding (I) can also be detected to  
 CC diagnose tumours. Agents which inhibit the activity of (I), especially  
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes  
 CC encoding (I), can be used to inhibit tumour growth, preferably by  
 CC inducing cell death. Methods from the present invention can be used to  
 CC identify compounds which inhibit the biological activity of (I). AAC58019  
 CC to AAC58102 represent PCR primers and hybridisation probes used in  
 CC examples from the present invention for human PRO sequences. AAC58103 to  
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and  
 CC protein sequences given in the exemplification of the present invention  
 XX  
 SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 2320; DB 3; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120

Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTGGAAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTGGAAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTACAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTACAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860

Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

# RESULT 2

AAA37101

ID AAA37101 standard; cDNA; 2320 BP.

XX

AC AAA37101;

XX

DT 08-AUG-2000 (first entry)

XX

DE Human PRO1780 (UNQ842) cDNA sequence SEQ ID NO:281.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200012708-A2.

XX

PD 09-MAR-2000.

XX

PF 01-SEP-1999; 99WO-US020111.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099536P.  
PR 09-SEP-1998; 98US-0099596P.  
PR 09-SEP-1998; 98US-0099598P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099792P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 10-SEP-1998; 98US-0099816P.  
PR 15-SEP-1998; 98US-0100385P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-0103314P.  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103395P.  
PR 07-OCT-1998; 98US-0103396P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.



PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.

PA (GETH ) GENENTECH INC.

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

DR WPI; 2000-237871/20.

DR P-PSDB; AAY99419.

PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
PT PRO polypeptides, useful for screening of potential peptide or small  
PT molecule inhibitors of the relevant receptor/ligand interactions.

PS Claim 2; Fig 159; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding then have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
CC primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention

Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2320; DB 3; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60  
|||||

Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

QY 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
|||||

Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy 121 GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
|||||

Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

QY            181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA    240  
             |||||

Db 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

**QY**

241 CAAAAGAGGTCTCTTTTATGCCAGATT TTA AAAAAGGAAGAAAAATCATATCAAGTTATCAG   300  

Db 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200

Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040

Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
 Qy 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100  
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 Db 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100  
 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
 ||||||||||||||||||||||||||||||||||||  
 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 3

AAF54401

ID AAF54401 standard; DNA; 2320 BP.  
 XX  
 AC AAF54401;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Primer #82 used in the identification of proteins.  
 XX  
 KW Secreted; transmembrane; gene therapy; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078961-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004342.  
 XX  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PT therapy.

XX

PS Example 82; Page 456; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy

XX

SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2320; DB 4; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480

Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320

Qy 1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380  
 |||  
 Db 1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380

Qy 1381 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440  
 |||  
 Db 1381 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440

Qy 1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500  
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 Db 1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500

Qy 1501 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560  
 |||  
 Db 1501 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560

Qy 1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620  
 |||  
 Db 1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620

Qy 1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680  
 |||  
 Db 1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680

Qy 1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740  
 |||  
 Db 1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740

Qy 1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTCTGCTA 1800  
 |||  
 Db 1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTCTGCTA 1800

Qy 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT 1860  
 |||  
 Db 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT 1860

Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920  
 |||  
 Db 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920

Qy 1921 TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980  
 |||  
 Db 1921 TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
 |||  
 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040

Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCCATATTCTTTCAGT 2100  
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCCATATTCTTTCAGT 2100

Qy 2101 TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2101 TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

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Db      2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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Qy      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
      |||
Db      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
      |||
Qy      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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Db      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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RESULT 4

ACD68440

ID ACD68440 standard; cDNA; 2320 BP.

XX

AC ACD68440;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; angiogenesis;  
 KW endothelial cell proliferation; wound healing; immune response;  
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
 KW cardiac insufficiency disorder; calcium flux; inflammation;  
 KW vascular endothelial growth factor-stimulated proliferation;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;  
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;  
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;  
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
 KW cartilage disorder; sports injury; arthritis; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073130-A1.

XX

PD 17-APR-2003.

XX

PF 11-DEC-2001; 2001US-00015869.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

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PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.



PR 10-SEP-1998; 98US-0099792P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 10-SEP-1998; 98US-0099816P.  
PR 15-SEP-1998; 98US-0100385P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
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PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
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PR 23-SEP-1998; 98US-0101476P.  
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PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
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PR 07-OCT-1998; 98US-0103395P.  
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PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.

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PR 14-OCT-1998; 98US-0104257P.  
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PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
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PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
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PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
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PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.



Db	121		GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301		TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301		TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Qy	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601		AATCCCCTTGCTTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601		AATCCCCTTGCTTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTG	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTG	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Db 961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020  
 Qy 1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTTCATTGGCCCAA 1080  
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 Db 1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680  
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Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
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Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
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RESULT 5

ACH04542

ID ACH04542 standard; cDNA; 2320 BP.

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AC ACH04542;

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DT 01-OCT-2003 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1780.

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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary;  
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;  
KW adrenal cortical capillary; endothelial cell growth; wound healing;  
KW stimulated T-lymphocyte proliferation; immune response suppression;  
KW neonatal heart hypertrophy; cardiac insufficiency disorder;  
KW vascular endothelial growth factor; inflammation; mononuclear cell;  
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;  
KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003044841-A1.

XX  
PD 06-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006856.  
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PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
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PR 02-SEP-1998; 98US-0098843P.  
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PR 03-NOV-1998; 98US-0106932P.  
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PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.



PR 17-NOV-1998; 98US-0108788P.  
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PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
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PR 30-DEC-1998; 98US-0114223P.  
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PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
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PR 04-SEP-2001; 2001US-00946374.

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PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

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DR WPI; 2003-492259/46.  
DR P-PSDB; ABO44514.  
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PT Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries and  
PT arthritis.

Query Match 100.0%; Score 2320; DB 8; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
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Qy    421 GTTGCA GTGAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 480
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Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600

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Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
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Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
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Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

ACD68086

ID ACD68086 standard; cDNA; 2320 BP.

XX

AC ACD68086;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

KW tissue typing; chromosome identification; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

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PD 17-APR-2003.

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PF 04-SEP-2001; 2001US-00946374.

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PR 24-AUG-2000; 2000WO-US023328.





Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCCTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCCTGATTGCTGAGAAGCT	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCCTGATTGCTGAGAAGCT	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200

Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040

Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 7

ADC18150

ID ADC18150 standard; cDNA; 2320 BP.

XX

AC ADC18150;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human PRO polynucleotide #80.

XX

KW Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;

KW gene mapping; genetic disorder.

XX

OS Homo sapiens.

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PN US2003064925-A1.

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PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00013907.

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PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;

XX

DR WPI; 2003-555602/52.

DR P-PSDB; ADC18151.

XX

PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.

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PS Claim 2; SEQ ID NO 281; 555pp; English.

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CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The sequences are useful in the preparation of a  
 CC medicament for treating a condition responsive to a PRO polypeptide. The  
 CC polypeptides are useful in a number of functional biological assays, as  
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCTTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCTTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900

Db	841	 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACCTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	 AGTACCACAAGACTTGGAGAACCTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740



Db	1681	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 8

ADD70796

ID ADD70796 standard; cDNA; 2320 BP.

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AC ADD70796;

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DT 15-JAN-2004 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003099625-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 12-DEC-2001; 2001US-00015386.  
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PR	03-NOV-1998;	98US-0106919P.

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PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX



Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380

Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		
	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1441		
	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501		
	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561		
	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621		
	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681		
	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741		
	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801		
	1801	ATTTTGGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861		
	1861	CTTGTCTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921		
	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981		
	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041		
	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101		
	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161		
	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA	2280

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280

QY      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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RESULT 9

ADD39873

ID ADD39873 standard; cDNA; 2320 BP.

XX

AC ADD39873;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003083462-A1.

XX

PD 01-MAY-2003.

XX

PF 10-DEC-2001; 2001US-00013913.

XX

PR 05-JAN-1999; 99WO-US000106.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.



PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-755122/71.  
 DR P-PSDB; ADD39874.  
 XX  
 PT New secreted and transmembrane PRO polypeptides useful for treating  
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or  
 PT hypo-insulinemia, sports injuries and arthritis.  
 XX  
 PS Claim 2; SEQ ID NO 281; 557pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 CC transmembrane protein) having at least 80% amino acid sequence identity  
 CC to an amino acid sequence chosen from 123 fully defined sequences as  
 CC given in the specification (including their extracellular domains either  
 CC or without their associated signal peptides. Also include are the  
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a  
 CC host cell comprising the vector, producing PRO, a chimaeric molecule  
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-  
 CC PRO antibody. Pro is useful as molecular weight markers for protein  
 CC electrophoresis and also for chromosome identification. PRO is also  
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation  
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is  
 CC useful for generating transgenic animals or knock-out animals which are  
 CC useful in development and screening useful reagents. PRO NA is also  
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are  
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410  
 CC polypeptides are useful for suppressing immune response. PRO1246  
 CC polypeptide is useful for treating cardiac insufficiency disorders.  
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and  
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human  
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474  
 CC polypeptides are useful for treating bone and/or cartilage disorders  
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418  
 CC polypeptides are useful for treating diabetes in skeletal muscle cells  
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for  
 CC treating Berger disease or other nephropathies associated with Schonlein-  
 CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's  
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,  
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present  
 CC sequence encodes a PRO protein of the invention.  
 XX  
 SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
      |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||
Db    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
      |||
Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
      |||
Db    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720

Qy    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
      |||
Db    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780

Qy    781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC 840
      |||
Db    781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC 840
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Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680

Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 10

ADD70319

ID ADD70319 standard; cDNA; 2320 BP.

XX

AC ADD70319;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003054406-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 06-DEC-2001; 2001US-00006818.  
 XX  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098723P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.  
 PR 09-SEP-1998; 98US-0099596P.  
 PR 09-SEP-1998; 98US-0099598P.  
 PR 09-SEP-1998; 98US-0099602P.  
 PR 09-SEP-1998; 98US-0099642P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099754P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099808P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 10-SEP-1998; 98US-0099815P.  
 PR 10-SEP-1998; 98US-0099816P.  
 PR 15-SEP-1998; 98US-0100385P.  
 PR 15-SEP-1998; 98US-0100388P.  
 PR 15-SEP-1998; 98US-0100390P.  
 PR 16-SEP-1998; 98US-0100584P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100661P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 16-SEP-1998; 98US-0100664P.  
 PR 17-SEP-1998; 98US-0100683P.  
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 PR 17-SEP-1998; 98US-0100710P.  
 PR 17-SEP-1998; 98US-0100711P.  
 PR 17-SEP-1998; 98US-0100919P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 18-SEP-1998; 98US-0100848P.  
 PR 18-SEP-1998; 98US-0100849P.  
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PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

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DR WPI; 2003-708344/67.

DR P-PSDB; ADD70320.

XX

PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
PT biological activity of cell, as molecular weight markers in protein  
PT electrophoresis, for treating arthritis, tumor.

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PS Claim 2; SEQ ID NO 281; 549pp; English.

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CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAACTTTAGGTGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCCTTCCTGATTGCTGAGAAGCT	540



Db	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380

Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280  
 |||  
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280

Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 11

ADD38440

ID ADD38440 standard; cDNA; 2320 BP.

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AC ADD38440;

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DT 15-JAN-2004 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

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OS Homo sapiens.

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PN US2003096955-A1.

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PD 22-MAY-2003.

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PF 07-DEC-2001; 2001US-00012755.

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PR 20-JUL-1999; 99US-0144758P.  
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PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.



Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGT CAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGT CAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGT CACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATT CAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATT CAGTTAAAGAAGCTCAAGGCAGA	1320
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Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGT CATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGT CATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTT CAGCA	1500
Db	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTT CAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTCTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTCTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920



Db	1861	 CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 12

ADD39396

ID ADD39396 standard; cDNA; 2320 BP.

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AC ADD39396;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003096954-A1.

XX

PD 22-MAY-2003.

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PF 07-DEC-2001; 2001US-00011671.

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PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	01-SEP-1998;	98US-0098749P.
PR	01-SEP-1998;	98US-0098750P.
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PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
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PR	17-NOV-1998;	98US-0108806P.
PR	17-NOV-1998;	98US-0108807P.

PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

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DR WPI; 2003-786999/74.

DR P-PSDB; ADD39397.

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PT Novel isolated PRO polypeptide useful for tissue typing, modulating

PT biological activity of cell, as molecular weight markers in protein  
PT electrophoresis, for treating arthritis, tumor.  
XX  
PS Claim 2; SEQ ID NO 281; 550pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTTGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
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Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 13

ADD38919

ID ADD38919 standard; cDNA; 2320 BP.

XX  
 AC ADD38919;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.  
 XX  
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003092061-A1.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 06-DEC-2001; 2001US-00007194.  
 XX  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098723P.  
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PR 18-NOV-1998; 98US-0108851P.  
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PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-765477/72.  
 DR P-PSDB; ADD38920.  
 XX  
 PT New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
 PT PRO1244, PRO1246, useful for treating cancerous tumors, cardiac  
 PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.  
 XX  
 PS Claim 2; SEQ ID NO 281; 555pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360

Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260

Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100

Db 2041 TGCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100  
 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
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 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
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RESULT 14

ADD40350

ID ADD40350 standard; cDNA; 2320 BP.

XX

AC ADD40350;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003082627-A1.

XX

PD 01-MAY-2003.

XX

PF 06-DEC-2001; 2001US-00006117.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

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 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-755104/71.  
 DR P-PSDB; ADD40351.  
 XX  
 PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,  
 PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac  
 PT insufficiency disorders.  
 XX  
 PS Claim 2; SEQ ID NO 281; 550pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
  
 Query Match 100.0%; Score 2320; DB 9; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTTAGA 60  
 Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
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 Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
 Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
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Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATAACAAGTCCGCGGCAGT	1380
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Qy	1381	GGCTGCCAGTGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
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Qy	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740

Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCA	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCA	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCAACCTCACTAA	2320

RESULT 15

ADE50571

ID ADE50571 standard; cDNA; 2320 BP.

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AC ADE50571;

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DT 29-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX  
OS Homo sapiens.  
XX  
PN US2003069179-A1.  
XX  
PD 10-APR-2003.  
XX  
PF 11-DEC-2001; 2001US-00015393.  
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PR 03-NOV-1998; 98US-0106932P.  
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PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
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PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
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PR 01-JUN-2001; 2001WO-US017800.  
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PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-708395/67.

DR P-PSDB; ADE50572.

XX

PT Novel secreted and transmembrane PRO polypeptides useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide and as therapeutic agents e.g. vaccines.

XX

PS Claim 2; SEQ ID NO 281; 555pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600



Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
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Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
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Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
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Db	901		AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
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Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
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Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
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Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280

Qy        2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
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Db        2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 06:50:49 ; Search time 190 Seconds  
(without alignments)  
6776.242 Million cell updates/sec

Title: US-10-017-867A-281  
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Scoring table: IDENTITY\_NUC  
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
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c	2	424.2	18.3	1056	4	US-09-833-381-631	Sequence 631, App
	3	382.4	16.5	470	4	US-09-833-381-348	Sequence 348, App
	4	143.2	6.2	2966	4	US-09-976-594-241	Sequence 241, App
	5	136.4	5.9	2107	3	US-09-180-852-1	Sequence 1, Appli
	6	136	5.9	1854	4	US-09-356-806-39	Sequence 39, Appl
	7	131.6	5.7	2092	4	US-09-356-806-7	Sequence 7, Appli
	8	128.4	5.5	1976	4	US-09-356-806-112	Sequence 112, App
	9	127.6	5.5	1413	4	US-09-813-918-1	Sequence 1, Appli
	10	118	5.1	2336	5	PCT-US92-00282-1	Sequence 1, Appli
	11	111.2	4.8	2339	5	PCT-US92-00282-2	Sequence 2, Appli

	12	95.6	4.1	735	4	US-09-305-856B-17	Sequence 17, Appl
	13	79.2	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
c	14	74	3.2	588	4	US-09-833-381-344	Sequence 344, App
	15	63.8	2.8	689	4	US-09-356-806-5	Sequence 5, Appli
	16	62.4	2.7	391	4	US-09-370-838-21	Sequence 21, Appl
	17	62.2	2.7	1591	4	US-09-356-806-44	Sequence 44, Appl
	18	56.8	2.4	1731	2	US-08-466-583-1	Sequence 1, Appli
	19	56.8	2.4	1731	4	US-08-265-427-1	Sequence 1, Appli
	20	56.8	2.4	1731	5	PCT-US95-07820-1	Sequence 1, Appli
	21	56.2	2.4	983	4	US-09-671-317-386	Sequence 386, App
	22	55	2.4	1602	4	US-09-356-806-117	Sequence 117, App
	23	53.4	2.3	783	5	PCT-US92-00282-22	Sequence 22, Appl
	24	49.2	2.1	657	4	US-09-669-751-104	Sequence 104, App
	25	48.6	2.1	1001	4	US-09-671-317-404	Sequence 404, App
	26	44.6	1.9	762	4	US-09-615-192A-218	Sequence 218, App
	27	43.6	1.9	1001	4	US-09-671-317-413	Sequence 413, App
	28	43.6	1.9	1001	4	US-09-671-317-414	Sequence 414, App
	29	43.6	1.9	1001	4	US-09-671-317-415	Sequence 415, App
	30	43.6	1.9	1001	4	US-09-671-317-417	Sequence 417, App
	31	43.6	1.9	1021	4	US-09-356-806-115	Sequence 115, App
	32	43.2	1.9	1001	4	US-09-671-317-416	Sequence 416, App
	33	42.6	1.8	2025	3	US-08-942-012B-23	Sequence 23, Appl
	34	42	1.8	1800	6	5180581-1	Patent No. 5180581
	35	42	1.8	2793	1	US-08-281-916-5	Sequence 5, Appli
	36	42	1.8	2793	2	US-08-460-725-7	Sequence 7, Appli
c	37	39.8	1.7	289	3	US-09-007-005-17	Sequence 17, Appl
c	38	39.8	1.7	289	3	US-09-244-796-17	Sequence 17, Appl
	39	39.6	1.7	50937	3	US-09-428-517-1	Sequence 1, Appli
	40	39.2	1.7	492	4	US-09-134-001C-808	Sequence 808, App
	41	39	1.7	759	4	US-09-305-856B-15	Sequence 15, Appl
	42	39	1.7	930	4	US-09-305-856B-13	Sequence 13, Appl
	43	39	1.7	1200	1	US-08-096-623A-19	Sequence 19, Appl
	44	38.8	1.7	474	4	US-09-621-976-18033	Sequence 18033, A
	45	38.8	1.7	11049	4	US-10-204-708-22	Sequence 22, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-833-381-210/c

; Sequence 210, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 210

; LENGTH: 883

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(883)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-210

Query Match 19.5%; Score 452.2; DB 4; Length 883;  
Best Local Similarity 83.8%; Pred. No. 2.2e-129;  
Matches 511; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy      331 ATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATTTGA 390
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Db      881 AATTAAGAAGCATTNTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATCTGA 822

Qy      391 AAAC TTATTAATGTTCTAGAACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAGAAA 450
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      821 AGCCCTTGTAAGCTAATGGAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAGAAA 762

Qy      451 GGATATCATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAACTTTTGA 510
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      761 GGATATAATGGATTCCCTTAAAGAATGAGAACTATGATCTGGTATTTGTTGAAGCATTGA 702

Qy      511 CTA CTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCAC 570
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      701 TTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAAACCATTTGTGGCCATTCTTTCCCAC 642

Qy      571 TTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCG 630
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      641 CACATTTCGGCTCTTTGGATTTTGGGCTACCAAGCCCCTTGTCTTATGTTCCAGTATTCCC 582

Qy      631 TTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTT 690
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      581 TTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTT 522

Qy      691 TAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACA 750
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Qy      751 TTTCACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTT 810
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Db      461 TTTCACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTT 402

Qy      811 CATTA ACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGT 870
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Db      401 TGTTA ACTCTGATTTTGCTTTGATTTTGCCCGGCCCTGCTTCCCAACACTGTTTATAT 342

Qy      871 TGGAGGCTTGATGGA AAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC 930
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Db      341 TGGAGGCTTGATGGA AAAACCTATTAAACCAGTACCACAAGTAAATAAACAGTTGGCATT 282

Qy      931 CAAGTTTGGG 940
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Db      281 CAGTTTGGG 272
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RESULT 2  
US-09-833-381-631/c



RESULT 3  
 US-09-833-381-348  
 ; Sequence 348, Application US/09833381  
 ; Patent No. 6672186  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
 ; FILE REFERENCE: 5800-119  
 ; CURRENT APPLICATION NUMBER: US/09/833,381  
 ; CURRENT FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 09/516,448  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 2050  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 348  
 ; LENGTH: 470  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(470)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-833-381-348

Query Match 16.5%; Score 382.4; DB 4; Length 470;  
 Best Local Similarity 95.9%; Pred. No. 5.6e-108;  
 Matches 446; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

Qy	963	CCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATG	1022
Db	1	CCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAGCAATG	60
Qy	1023	CCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAG	1082
Db	61	CCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAG	120
Qy	1083	ATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGG	1142
Db	121	ATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGG	180
Qy	1143	CTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCA	1202
Db	181	CTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCA	240
Qy	1203	TCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGG	1262
Db	241	TCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGG	300
Qy	1263	TCCGAGTAGAAGCCAAAAAG-TTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG	1321
Db	301	TCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG	360
Qy	1322	ACATTGGCTC-TTAAGATGAAACAAATCATGG--AAGACAAGAGATACAAGTCCGC-GGC	1377
Db	361	ACATTGGCTCTTTAAGATGAAACAAATCATGGGAAGGACAAGAGATACAAGTCCGC	420



Qy 1378 AGTGGCT--GCCAGTGTTCATCTGCGCTCCACCCGCTCAGCCCC 1420  
 ||||| | | ||||| ||||| |||||  
 Db 421 AGTGGCTTGCCAGTGTTCNTCCTGCGTTCCACCCGTTAGGCCC 465

RESULT 4

US-09-976-594-241

; Sequence 241, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 241

; LENGTH: 2966

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. 6673549 997080.1

US-09-976-594-241

Query Match 6.2%; Score 143.2; DB 4; Length 2966;

Best Local Similarity 48.3%; Pred. No. 2.2e-33;

Matches 542; Conservative 0; Mismatches 553; Indels 27; Gaps 4;

Qy 437 TTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATA 496  
 ||| | | | || | || | || | ||| ||| | |||  
 Db 411 TTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTT 470  
 Qy 497 GTTGAAACTTTTGACTACTGTCCCTTTCCTGATTGCTGAGAAGCTTGGAAGCCATTTGTG 556  
 | || || | ||| ||||| ||||| ||||| || |||||  
 Db 471 ATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCACTCCCTTTTGTG 530  
 Qy 557 GCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGG-----GCTACCAATC 604  
 || ||| | ||| | || | ||||  
 Db 531 CTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCT 590  
 Qy 605 CCCTTGCTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGC 664  
 || | || ||||| || || | || || || || || || ||  
 Db 591 CCACTTTCCTATGTACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAA 650  
 Qy 665 CGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCT 724  
 |||| | |||| | || | || | || | || | || | ||  
 Db 651 AGAGTAAAAAATCAATGCTTTCAGTTTGTTCCACTTCTGGATTACGACTAT 710  
 Qy 725 ACATTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCAT 784  
 ||| | | | | || | || | || | || | || | ||

Db	711	CATTTTTGGGAAGAGTTTATTAGTAAGGCATTAGGAAGGCCCACTACA---TTATGTGAG	767
Qy	785	CTTCTACTGAAAGCAGAGTTGTGGTTCATTA ACTCTGACTTTGCCTTTGATTTTGCTCGA	844
Db	768	ACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCTCAA	827
Qy	845	CCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTA	904
Db	828	CCATACCAACCTA ACTTTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTG	887
Qy	905	CCACAAGACTTGGAGA ACTTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGTGACC	964
Db	888	CCTAAGGAAATGGAAAATTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGT TTTTCT	947
Qy	965	TTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCC	1024
Db	948	CTGGGGTCACTGTTTCAA AATGTTACAGA---AGAAAAGGCTAATATCATTTGCTTCAGCC	1004
Qy	1025	TTTGCTCACCTACCCCCAAGGGGTGATATGGAAGTGT CAGTGTTCTCATTGGCCCAAAGAT	1084
Db	1005	CTTGCCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAAAACCATCCACA---	1061
Qy	1085	GTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCT	1144
Db	1062	-----TTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGT	1115
Qy	1145	CACCCAAGCATCCGTCTGTTTGT CACCCACGGCGGGCAGAATAGCATAATGGAGGCCATC	1204
Db	1116	CATCCCAAAACCAAAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAAGCTATT	1175
Qy	1205	CAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTC	1264
Db	1176	TACCATGGGGTCCCTATGGTGGGAGTCCCATATTTGGTGATCAGCTTGATAACATAGCT	1235
Qy	1265	CGAGTAGAAGCCAAAAAGTTTGGTGT TTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACA	1324
Db	1236	CACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAGCGAAGAT	1295
Qy	1325	TTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCT	1384
Db	1296	TTACTGAGGGCTTTTGAGAACAGTCATTACCGATT CCTCTTATAAAGAGAATGCTATGAGA	1355
Qy	1385	GCCAGTGT CATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATT	1444
Db	1356	TTATCAAGAATTCAACATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATC	1415
Qy	1445	GACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCC	1504
Db	1416	GAGTTTGT CATGCGCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACC	1475
Qy	1505	TGGCATGAGCAGTACCTGTTCTGACGTTTTTTGTGTTTCTGCTG	1546
Db	1476	TGGTTCAGCACTACTCTATAGATGTGATTGGGTTCCTGCTG	1517



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Db      966 TGTGGTGTCTTCTCTGGGGTCGATGATCAGTAAC---ATGTCAGAAGAAAGTGCCAACAT 1022
Qy      1012 GATGAACAATGCCTTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCACTGTTCTCA 1071
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1023 GATTGCATCAGCCCTTGCCCAGATCCACAAAAGGTTCTATGGA-----GATTGA 1073
Qy      1072 TTGGCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAG 1131
      || || || || || || || || || || || || || || || || || || || || ||
Db      1074 TGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTATAAGTGGTTACCCCAGAA 1133
Qy      1132 TGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCAT 1191
      ||||| || | ||| || | || | || | || | || | || | || | || | || | || |
Db      1134 TGACCTTCTTGGTCATCCCAAACCAAAGCTTTTATAACTCATGGTGGGAACCAATGGCAT 1193
Qy      1192 AATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCC 1251
      ||||| ||| | ||||| | || ||||| || || || || || || || || || || ||
Db      1194 CTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTTGC GGATCAACA 1253
Qy      1252 TGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTCTATTCACTTAAAGAAGCT 1311
      ||| ||||| | | | ||||| | | | || | | || | || | || | || | || |
Db      1254 TGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACATCAGGACCAT 1313
Qy      1312 CAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTC 1371
      ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1314 GTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTATCTATAAAGA 1373
Qy      1372 CGCGGCAGTGGCTGCCAGTGTCTCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCT 1431
      || || || | || || || || || || || || || || || || || || || || ||
Db      1374 GAATATCATGAAATTATCAAGAATTCATCATGATCAACCGGTGAAGCCCTGGATCGAGC 1433
Qy      1432 GGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGT 1491
      || ||||| |||| ||| || || || || || || || || || || || || || || ||
Db      1434 AGTCTTCTGGATTGAGTTTGTCTGCGCCATAAAGGAGCCAAGCACCTTCGGGTCGCAGC 1493
Qy      1492 CTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547
      | | | |||| || | || || || || || || || || || || || || || || ||
Db      1494 CCACAACCTCACCTGGATCCAGTACCACTCTTTGGATGTGATAGCATTCCTGCTGG 1549

```

# RESULT 6

US-09-356-806-39

; Sequence 39, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 39
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)...(1584)
US-09-356-806-39
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Query Match          5.9%; Score 136; DB 4; Length 1854;
Best Local Similarity 49.6%; Pred. No. 2.7e-31;
Matches 469; Conservative 0; Mismatches 460; Indels 17; Gaps 4;
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Qy      603 TCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGG 662
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Db      580 TCCCTCCTTCCTACGTACCTGTTGTTATGTGAGAATTAAGTATCAAATGACTTTCATGG 639

Qy      663 GCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAG 721
      | || || ||| | | ||| ||||| |||  |  |  ||
Db      640 AGAGGGTAAAAAATATGATCTATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACA 699

Qy      722 TCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCT 781
      | | | || || || | | | | ||| |||| | |  |  ||||
Db      700 TGAAGAAGTGGGATCAGTTTTATAGTGAAGTTCTAGGAAGACCC-----ACTACATTATCT 755

Qy      782 CATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAAGTCTGACTTTGCCTTTGATTTTGCT 841
      |  |  ||||| || | ||| | |||  ||  ||| | ||| |
Db      756 GAGACAATGGGGAAAGCTGACGTATGGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCA 815

Qy      842 CGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCA 901
      || || | || || | || ||||| |||  |||||  |||||
Db      816 TATCCACTCTTACCAAATGTTGATTTTGTGGAGGACTCCACTGCAAACCTGCCAAACCC 875

Qy      902 GTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTG 961
      | || | || || ||| ||| | | ||| || ||||| ||| |
Db      876 CTGCCCTAAGGAAATGGAAGACTTTGTACAGAGCTCTGGAGAAAATGGTGTGTGGTGTGTT 935

Qy      962 ACCTTGCGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAAT 1021
      |  |||| || |||| | | |  ||  ||||  ||| | ||
Db      936 TCTCTGGGGTCAATGGTCAGTAAC---ATGACAGAAGAAAGGGCCAACGTAATTGCATCA 992

Qy      1022 GCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA 1081
      ||| | || || | || ||| ||| | ||||  | | | ||| |||
Db      993 GCCCTGGCCCAGATCCCAAAAAGGTTCTGTGGA-----GATTGATGGGAATAAA 1043

Qy      1082 GATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTG 1141
      |  |  || | |||  |||  |  ||| | || ||||| |||
Db      1044 CCAGATACCTTAGGTCTCAATACTCGGCTCTACAAGTGGATACCCCAAGATGACCTTCTA 1103

Qy      1142 GCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCC 1201
      | ||| |||| | | | ||| | || || |||  ||| ||||  |||||
Db      1104 GGTCAATCAAAGACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTACGAGGCA 1163

Qy      1202 ATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATG 1261
      ||| | |||| | || ||||| ||| || ||||  |||||  |||||
Db      1164 ATCTACCATGGGATCCCTATGGTGGGGATTCCATTGTTTGCCGATCAACCTGATAACATT 1223
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Qy      1262 GTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG 1321
          | | | | | | | | | | | | | | | | | |
Db      1224 GCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTGGACTTCAACACAATGTCGAGTACA 1283

Qy      1322 ACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTG 1381
          ||| | | | | | | | | | | | | | | |
Db      1284 GACTTGCTGAATGCATTGAAGAGAGTAATTAATGATCCTTCATATAAAGAGAATGTTATG 1343

Qy      1382 GCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGG 1441
          || | | | | | | | | | | | | | | |
Db      1344 AAATTATCAAGAATTCAACATGATCAACCAAGTGAAGCCCCTGGATCGAGCAGTCTTCTGG 1403

Qy      1442 ATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAG 1501
          |||| | | | | | | | | | | | | | |
Db      1404 ATTGAATTTGTCATGCGCCACAAAGGAGCTAAACACCTTCGGGTTGCAGCCCACGACCTC 1463

Qy      1502 CCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547
          |||| | | | | | | | | | | | |
Db      1464 ACCTGGTTCAGTACCCTCTTTGGATGTGATTGGGTTCCCTGCTGG 1509

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RESULT 7

US-09-356-806-7

; Sequence 7, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 2092

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (38)...(1621)

US-09-356-806-7

Query Match 5.7%; Score 131.6; DB 4; Length 2092;

Best Local Similarity 49.2%; Pred. No. 6.8e-30;

Matches 470; Conservative 0; Mismatches 469; Indels 17; Gaps 4;

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Qy      593 GGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATG 652
          || || | ||| || |||| || || | || || || ||
Db      593 GGAATTCTGTTCCCTCCTTCCTATGTGCCTGTTGTTATGTCAGAACTAAGTGACCAAATG 652

Qy      653 GACTTCTGGGGCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACA 711

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Db	653	ACTTTCATAGAGAGGGTAAAAAATATGATCTATGTGCTTTATTTTGAATTTTGGTTCCAA	712
Qy	712	GCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCC	771
Db	713	ATATTTGACATGAAGAAGTGGGATCAGTTCTACAGTGAAGTTCTAGGAAGACCC----AC	768
Qy	772	AGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTT	831
Db	769	TACGTTATCTGAGACAATGGCAAAGCTGACATATGGCTTATTCGAAACTACTGGGATTT	828
Qy	832	TGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACC	891
Db	829	TCAATTTCCCTCACCACCTCTTACCAAATGTTGAGTTCGTTGGAGGACTCCACTGCAAACC	888
Qy	892	TATTAAACCAGTACCACAAGACTTGGAGAACCTTCATTGCCAAGTTTGGGGACTCTGGTTT	951
Db	889	TGCCAAACCCCTACCGAAGGAAATGGAAGAGTTTGTCCAGAGCTCTGGAGAAAATGGTGT	948
Qy	952	TGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGA	1011
Db	949	TGTGGTGTTTTCTCTGGGGTCGATGGTCAGTAAC---ACGTCAGAAGAAAGGGCCAATGT	1005
Qy	1012	GATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCA	1071
Db	1006	AATTGCATCAGCCCTTGCCAAGATCCCAAAAAGGTTCTGTGGA-----GATTTGA	1056
Qy	1072	TTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCCTCAGAG	1131
Db	1057	TGGGAATAAACCAGATACTTTAGGACTCAATACTCGGCTGTACAAGTGGATACCCAGAA	1116
Qy	1132	TGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCAT	1191
Db	1117	TGATCTTCTTGGTCACCCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCAT	1176
Qy	1192	AATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTGGAGACCAGCC	1251
Db	1177	CTATGAGGCAATCTACCATGGAATCCCTATGGTGGGCGTTCCATTGTTGCAGATCAACC	1236
Qy	1252	TGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAGTTAAAGAAGCT	1311
Db	1237	TGATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTAGTTTGGACTTCCACACAAT	1296
Qy	1312	CAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTC	1371
Db	1297	GTCGAGTACAGACTTACTCAATGCACTGAAGACAGTAATTAATGATCCTTTATATAAAGA	1356
Qy	1372	CGCGGCAGTGGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCT	1431
Db	1357	GAATGCTATGAAATTATCAAGAATTCATCATGATCAACCAGTGAAGCCCCCTTGATCGAGC	1416
Qy	1432	GGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGT	1491
Db	1417	AGTCTTCTGGATTGAATTTGTGATGCGCCATAAAGGAGCCAAGCACCTTCGGGTTGCAGC	1476
Qy	1492	CTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG	1547

Db 1477 CCACGACCTCACCTGGTTCAGTACCACTCTTTGGATGTGACTGGGTTCCCTGCTGG 1532

US-09-356-806-112

; Patent No. 6586175

; APPLICANT: Penny, Laura

; APPLICANT: Miller, Andrew

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and

; FILE REFERENCE: SEO-22PRV2

; CURRENT FILING DATE: 1999-07-20

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; SOFTWARE: FastSEQ for Windows Version 3.0
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; LENGTH: 1976

; ORGANISM: H. sapiens

; NAME/KEY: CDS

US-09-356-806-112

Best Local Similarity 49.0%; Pred. No. 6.4e-29;

Qy 593 GGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATG 652

QY 653 GACTTCTGGGGCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACA 711

QY 712 GCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTCACAGAAGGCTCTAGGCC 771

QY 772 AGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTT 831

Qy 832 TGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACC 891  
||| ||| |||| || | ||| || ||| ||| ||||| ||| |||||

Qy           892 TATTAAACAGTACCACAAGACTTTGGAGAAGTTTCATTGCCAAGTTTTGGGGACTCTGGTTT 951  
             | | | | | | | | | | | | | | | | | | | | | | | |



Qy 952 TGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGA 1011  
 ||| | | | |||| | | | | | | | | | | |||| | |  
 Db 925 TGTGGTGTCTTCTCTGGGGTCGATGATCAGTAAC---ATGTCAGAAGAAAGTGCCAACAT 981  
 Qy 1012 GATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCA 1071  
 ||| | | | |||| | | | | | | | | | | | | | |  
 Db 982 GATTGCATCAGCCCTTGCCCAGATCCACAAAAGGTTCTATGGA-----GATTTGA 1032  
 Qy 1072 TTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAG 1131  
 | | | | | | | | | | | | | | | | | | | |  
 Db 1033 TGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTACAAGTGGTTACCCAGAA 1092  
 Qy 1132 TGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCAT 1191  
 ||||| | | | | | | | | | | | | | | | | | | |  
 Db 1093 TGACCTTCTTGGTCATCCCAAACCAAAGCTTTTATAACTCATGGTGAACCAATGGCAT 1152  
 Qy 1192 AATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCC 1251  
 ||||| | | | | | | | | | | | | | | | | | | |  
 Db 1153 CTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTCGGGATCAACA 1212  
 Qy 1252 TGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAGTTAAAGAAGCT 1311  
 ||| |||| | | | | |||| | | | | | | | | | |  
 Db 1213 TGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACATCAGGACCAT 1272  
 Qy 1312 CAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTC 1371  
 ||| | | | | | | | | | | | | | | | |  
 Db 1273 GTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTGTCTATAAAGA 1332  
 Qy 1372 CGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCT 1431  
 | | | | | | | | | | | | | | | | | |  
 Db 1333 GAATGTCATGAAATTATCAAGAATTCATCATGACCAACCAATGAAGCCCCTGGATCGAGC 1392  
 Qy 1432 GGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGT 1491  
 || | ||||| | | | | | | | | | | | | | |  
 Db 1393 AGTCTTCTGGATTGAGTTTGTCTGCGCCACAAAGGAGCCAAGCACCTTCGAGTCGCAGC 1452  
 Qy 1492 CTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547  
 | | | |||| | | | | | | | | | | | | | |  
 Db 1453 TCACAACCTCACCTGGATCCAGTACCCTCTTTGGATGTGATAGCATTCCTGCTGG 1508

RESULT 9

US-09-813-918-1

; Sequence 1, Application US/09813918

; Patent No. 6383789

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001175

; CURRENT APPLICATION NUMBER: US/09/813,918

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1  
; LENGTH: 1413  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-918-1

Query Match 5.5%; Score 127.6; DB 4; Length 1413;  
Best Local Similarity 50.1%; Pred. No. 8.9e-29;  
Matches 378; Conservative 0; Mismatches 364; Indels 12; Gaps 2;

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QY      794 AAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTT 853
      ||||| || | ||| || | || || || || || || || ||
Db      551 AAAGCTGACATATGGCTTATGCGAAACCCCTGGAGTTTTCAATTTCCCTCATCCATTCTTA 610

QY      854 CCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGAC 913
      || ||| || || ||||| || || || || || || || ||
Db      611 CCAAACGTTGATTTTGTGGAGGATTCCACTGCAAACCTGCCAAACCCCTACCTAAGGAA 670

QY      914 TTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCC 973
      ||||| || || | || || || || || || || || || ||
Db      671 ATGGAGGAGTTTGTACAGAGCTCTGGAGAAAATGGTGTGTGGTGTCTCTGGGGTCA 730

QY      974 ATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCAC 1033
      || | | | | || | || || || || || || || || ||
Db      731 GTGATAAGTAAC---ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAGG 787

QY      1034 CTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTTGGCCCAAAGATGTCCACCTG 1093
      | || ||| || | || || || || || || || || || ||
Db      788 ATCCCACAAAAGGTTCTGTGGA-----GATTTGACGGGAATAAACAGATGCCTTA 838

QY      1094 GCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGC 1153
      | | ||| | | || | || | || || || || || || ||
Db      839 GGTCTCAATACTCGGCTGTACAAGTGGATACCCCAAGATGACCTTCTAGGTATCCAAA 898

QY      1154 ATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGT 1213
      | | | ||| || || || || || || || || || || || ||
Db      899 ACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGG 958

QY      1214 GTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAA 1273
      | ||||| || || || || || || || || || || || ||
Db      959 ATCCCATGGTGGGCATTCCATTGTTTTTTGATCAACCTGATAACATTGCTCACATGAAG 1018

QY      1274 GCCAAAAGTTTGGTGTCTTCTATTCAAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 1333
      |||| | || || | || || || || || || || || ||
Db      1019 GCCAAGGGAGCAGCTGTTAGATTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAAT 1078

QY      1334 AAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTC 1393
      |||| | | || | || || || || || || || || ||
Db      1079 GCACTGAAGACAGTAATTAATGATCCTTTATATAAAGAGAATATTATGAAATTATCAAGA 1138

QY      1394 ATCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTC 1453
      || | | || || || || || || || || || || || ||
Db      1139 ATTCAACATGATCAACCAGTAAAGCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTC 1198

QY      1454 CTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAG 1513
      | | || || || || || || || || || || || || ||
Db      1199 ATGCCCCACAAAGGAGCCAAACACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAG 1258
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Qy 1514 CAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547  
 | | | | | | | | | | | | | | | | | |  
 Db 1259 TACCACTCTTTGGATGTGATTGGGTTTCTGCTGG 1292

RESULT 10

PCT-US92-00282-1

; Sequence 1, Application PC/TUS9200282  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OWENS, IDA S.  
 ; APPLICANT: RITTER, JOSEPH K.  
 ; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION  
 ; TITLE OF INVENTION: THEREIN.  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; STREET: 1615 L STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20036-5601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US92/00282  
 ; FILING DATE: 19920110  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SCOTT, WATSON T.  
 ; REGISTRATION NUMBER: 26581  
 ; REFERENCE/DOCKET NUMBER: 91532-PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3000  
 ; TELEFAX: 202-822-0944  
 ; TELEX: 6714627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2336 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 PCT-US92-00282-1

Query Match 5.1%; Score 118; DB 5; Length 2336;  
 Best Local Similarity 47.6%; Pred. No. 1.2e-25;  
 Matches 457; Conservative 0; Mismatches 485; Indels 18; Gaps 3;

Qy 599 CCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTC 658  
 | | | | | | | | | | | | | | | | | |  
 Db 559 CCCAACCATTCTCTACGTGCCAGGCCCTCTCTCTCTCATTGAGATCACATGACCTTC 618  
 Qy 659 TGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATG 718

Db	619	CTGCAGCGGGTGAAGAACATGCTCATTGCCTTTTCACAGAACTTTCTGTGCGACGTGGTT	678
Qy	719	CAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTG	778
Db	679	TATCCCCGPTATGCAACCCTTGCCTCAGAATTCCTTCAGAGAG-----AGGTGACTGTC	732
Qy	779	TCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTT	838
Db	733	CAGGACCTATTGAGCTCTGCATCTGTCTGGCTGTTTAGAAGTGACTTTGTGAAGGATTAC	792
Qy	839	GCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAA	898
Db	793	CCTAGGCCCATCATGCCCAATATGTTTTTGTGGTGAATCAACTGCCTTCACCAAAT	852
Qy	899	CCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTT	958
Db	853	CCACTATCCCAGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAATTGTGGTT	912
Qy	959	GTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAAC	1018
Db	913	TTCTCTTTGGGATCAATGGTCTCAGAAATTCAGAAA---GAAGAAAGCTATGGCAATTGCT	969
Qy	1019	AATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCC	1078
Db	970	GATGCTTTGGGCAAAATCCCTCAGACAGTCCTGTGGCGGTACACTGGAACCCGACCATCG	1029
Qy	1079	AAAGATGTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTC	1138
Db	1030	AATCTTGCGAAC-----AACACGATACCTGTAAAGTGGCTACCCCAAACGATCTG	1080
Qy	1139	CTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAG	1198
Db	1081	CTTGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTCCCATGGTGTATTATGAA	1140
Qy	1199	GCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAAC	1258
Db	1141	AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTGGTGATCAGATGGACAAT	1200
Qy	1259	ATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCA	1318
Db	1201	GCAAAGCGCATGGAGACTAAGGGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCT	1260
Qy	1319	GAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCA	1378
Db	1261	GAAGATTTAGAAAATGCTCTAAAAGCAGTCATCAATGACAAAAGTTACAAGGAGAACATC	1320
Qy	1379	GTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGTGGTGGGC	1438
Db	1321	AGGCGCCTCTCCAGCCTTCACAAGGACCGCCCGGTGGAGCCGCTGGACCTGGCCGTGTTT	1380
Qy	1439	TGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAG	1498
Db	1381	TGGGTGGAGTTTGTGATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGAGCCCACGAC	1440
Qy	1499	CAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTG	1558

Db 1441 CTCACCTGGTACCAGTACCATTCCTTGGACGTGATTGGTTTCCTCTTGGCCGTCGTGCTG 1500

RESULT 11

PCT-US92-00282-2

; Sequence 2, Application PC/TUS9200282  
; GENERAL INFORMATION:  
; APPLICANT: OWENS, IDA S.  
; APPLICANT: RITTER, JOSEPH K.  
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION  
; TITLE OF INVENTION: THEREIN.  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1615 L STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/00282  
; FILING DATE: 19920110  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SCOTT, WATSON T.  
; REGISTRATION NUMBER: 26581  
; REFERENCE/DOCKET NUMBER: 91532-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2339 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US92-00282-2

Query Match 4.8%; Score 111.2; DB 5; Length 2339;  
Best Local Similarity 48.5%; Pred. No. 1.5e-23;  
Matches 376; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

Qy	783	ATCTTCTACTGAAAGCAGAGTTGTGGTTCATTA	ACTCTGACTTTGCCTTTGATTTTGCTC	842
Db	740	ATCTTGTGTCAGCTATGCATCCGTGTGGCTGTTCCGAGGGGACTTTGTGATGGACTACCCCA		799
Qy	843	GACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGAAAAACCTATTAAACCAG		902
Db	800	GGCCGATCATGCCCAACATGGTCTTCATTGGGGGCATCAACTGTGCCAACGGGAAGCCAC		859



; PRIOR APPLICATION NUMBER: 60/084,807  
 ; PRIOR FILING DATE: 1998-05-07  
 ; NUMBER OF SEQ ID NOS: 124  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 17  
 ; LENGTH: 735  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(735)  
 US-09-305-856B-17

Query Match 4.1%; Score 95.6; DB 4; Length 735;  
 Best Local Similarity 50.2%; Pred. No. 4.5e-19;  
 Matches 236; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy	1089	ACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACC	1148
Db	167	ATCTTGCGAACAAACACGATACTTGTTAAGTGGCTACCCCAAACGATCTGCTTGGTCACC	226
Qy	1149	CAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGC	1208
Db	227	CGATGACCCGTGCCTTTATCACCCATGCTGGTTCCCATGGTGT'TATGAAAGCATATGCA	286
Qy	1209	ATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAG	1268
Db	287	ATGGCGTTCCTCATGGTGTATGATGCCCTTGTTTGGTGATCAGATGGACAATGCAAAGCGCA	346
Qy	1269	TAGAAGCCAAAAAGTTTGGTGT'TTCTATTAGTTAAAGAAGCTCAAGGCAGAGACAT'TGG	1328
Db	347	TGGAGACTAAGGGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAAGATT'TAG	406
Qy	1329	CTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCA	1388
Db	407	AAAATGCTCTAAAAGCAGTCATCAATGACAAAAGTTACAAGGAGAACATCATGCGCCTCT	466
Qy	1389	GTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACC	1448
Db	467	CCAGCCTTCACAAGGACCGCCCGGTGGAGCCGCTGGACCTGGCCGTGTTCTGGGTGGAGT	526
Qy	1449	ACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGC	1508
Db	527	TTGTGATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGAGCCACGACCTCACCTGGT	586
Qy	1509	ATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTG	1558
Db	587	ACCAGTACCATTCTTGGACGTGATTGGTTTCTCTTGGCCGTCGTGCTG	636

RESULT 13

US-08-232-463-14  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEIFLINGER, F.





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Qy      1859 CTCTTGTCTCCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA 1918
          :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      1220 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1279

Qy      1919 CTTGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTC 1978
          :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      1280 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1339

Qy      1979 TCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACT 2038
          :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      1340 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1399

Qy      2039 CCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCA 2098
          :::: ::::: ::::: ::::: ::::: ::::: ::::: | | | | | | | | | |
Db      1400 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAA 1459

Qy      2099 GTTCTGTCTTTGTT 2112
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# RESULT 14

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US-09-833-381-344/c
; Sequence 344, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-344

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Best Local Similarity 61.3%; Pred. No. 1.9e-12;
Matches 119; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

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Qy      1100 AATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGT 1159
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Db      564 AATACGAGAGTGTACAAGTGGCTCCCCAGAATGACCTCCTTGGTCATCAAAAACAAA 505

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Qy      1220 ATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAA 1279
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and

Best Local Similarity 60.8%; Pred. No. 3e-09;

|||||    |||||    |    |    |||    |||    |||    |||    |||    |||

Search completed: May 16, 2004, 14:05:18

Job time : 194 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 07:14:19 ; Search time 1397 Seconds  
(without alignments)  
7536.345 Million cell updates/sec

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Perfect score: 2320  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result                      %  
Query

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2	2320	100.0	2320	12	US-10-015-395A-281	Sequence 281, App
3	2320	100.0	2320	13	US-10-006-485A-281	Sequence 281, App
4	2320	100.0	2320	13	US-10-013-907A-281	Sequence 281, App
5	2320	100.0	2320	13	US-10-015-499A-281	Sequence 281, App
6	2320	100.0	2320	13	US-10-226-254A-281	Sequence 281, App
7	2320	100.0	2320	15	US-10-006-856A-281	Sequence 281, App
8	2320	100.0	2320	15	US-10-006-818A-281	Sequence 281, App
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#### ALIGNMENTS

RESULT 1  
 US-09-946-374-281  
 ; Sequence 281, Application US/09946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
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Query Match 100.0%; Score 2320; DB 10; Length 2320;  
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
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Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100

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Qy      2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy      2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA 2280

Qy      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
         |||||||||||||||||||||||||||||||||||
Db      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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RESULT 2

US-10-015-395A-281

; Sequence 281, Application US/10015395A

; Publication No. US20040073015A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C57

; CURRENT APPLICATION NUMBER: US/10/015,395A

; CURRENT FILING DATE: 2001-12-12

; Prior application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-395A-281

Query Match 100.0%; Score 2320; DB 12; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960

Db	901	 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCTCATTGGCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800

Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATGGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATGGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 3

US-10-006-485A-281

; Sequence 281, Application US/10006485A

; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C9  
; CURRENT APPLICATION NUMBER: US/10/006,485A  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
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; PRIOR FILING DATE: 1998-09-29



; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
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; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2320; DB 13; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
      |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGCACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||
Db    481 CTTGCACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
```

Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 4

US-10-013-907A-281

; Sequence 281, Application US/10013907A

; Publication No. US20030064925A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C34

; CURRENT APPLICATION NUMBER: US/10/013,907A

; CURRENT FILING DATE: 2001-12-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-013-907A-281

Query Match 100.0%; Score 2320; DB 13; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60  
|  
Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60  
  
Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
|  
Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
  
Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
|  
Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
  
Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240  
|  
Db 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240  
  
Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Db	241	 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Db	541	 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	 AATCCCCTTGTCTTATGTTCCAGTATTCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140

Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980

Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 5

US-10-015-499A-281

; Sequence 281, Application US/10015499A

; Publication No. US20030065142A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C42

; CURRENT APPLICATION NUMBER: US/10/015,499A

; CURRENT FILING DATE: 2001-12-11

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-499A-281



Query Match 100.0%; Score 2320; DB 13; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCA GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
      |||
Db    421 GTTGCA GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||
Db    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
      |||
Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
      |||
Db    661 GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720

Qy    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
      |||
Db    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCCTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCCTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680

Db	1621		AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681		TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681		TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801		ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801		ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861		CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861		CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921		TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921		TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981		CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981		CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCACT	2100
Db	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCACT	2100
Qy	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 6

US-10-226-254A-281

; Sequence 281, Application US/10226254A

; Publication No. US20030224478A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-226-254A-281

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Query Match          100.0%; Score 2320; DB 13; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
        |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        |||

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Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTCAAGTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTCAAGTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860

Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

# RESULT 7

US-10-006-856A-281

; Sequence 281, Application US/10006856A

; Publication No. US20030044841A1

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C14

; CURRENT APPLICATION NUMBER: US/10/006,856A

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 477  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 281  
; LENGTH: 2320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-006-856A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		GGCTGCCAGTGTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441		GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441		GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

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; Sequence 281, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-818A-281

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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200

Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGTCATATTCTTTCAGT	2100

Db	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 9

US-10-015-393A-281

; Sequence 281, Application US/10015393A

; Publication No. US20030069179A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C46

; CURRENT APPLICATION NUMBER: US/10/015,393A

; CURRENT FILING DATE: 2002-06-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-393A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGCTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGCTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900

Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740



Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 10

US-10-015-869A-281

; Sequence 281, Application US/10015869A

; Publication No. US20030073130A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-281

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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
        |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        |||
Db    241 CAAAAGAGGTCCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
        |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
        |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
        |||
Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

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Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCTACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCTACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280

Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280

Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
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Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 11

US-10-012-121A-281

; Sequence 281, Application US/10012121A

; Publication No. US20030073810A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C20

; CURRENT APPLICATION NUMBER: US/10/012,121A

; CURRENT FILING DATE: 2001-12-07

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-121A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60  
 |||

Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120  
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Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180  
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Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCA 240  
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Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080

Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980  
 |||||  
 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980  
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
 |||||  
 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
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 Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100  
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100  
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 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220  
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
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 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280  
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320  
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RESULT 12

US-10-006-116A-281

; Sequence 281, Application US/10006116A

; Publication No. US2003008262A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C15

; CURRENT APPLICATION NUMBER: US/10/006,116A

; CURRENT FILING DATE: 2001-12-16

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01



; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
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; PRIOR APPLICATION NUMBER: 60/098843  
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; PRIOR FILING DATE: 1998-09-29  
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; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882

; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2320; DB 15; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780

Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441		GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCTAGCA	1500
Db	1441		GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCTAGCA	1500
Qy	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561		GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620

Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 13

US-10-006-117A-281

; Sequence 281, Application US/10006117A

; Publication No. US20030082627A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-117A-281

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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        |||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        |||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        |||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        |||||||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
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Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260



Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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RESULT 14

US-10-017-527A-281

; Sequence 281, Application US/10017527A

; Publication No. US20030082628A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C63

; CURRENT APPLICATION NUMBER: US/10/017,527A

; CURRENT FILING DATE: 2001-12-13

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536

; PRIOR FILING DATE: 1998-09-09

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; PRIOR FILING DATE: 1998-09-17  
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; PRIOR FILING DATE: 1998-09-23  
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; PRIOR APPLICATION NUMBER: 60/101738  
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; PRIOR FILING DATE: 1998-09-29  
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; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
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; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960

Db	901	 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
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Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800

Db 1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800  
 Qy 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860  
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 Db 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860  
 Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920  
 Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980  
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980  
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 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040  
 Qy 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100  
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 Db 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100  
 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160  
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RESULT 15

US-10-013-913A-281

; Sequence 281, Application US/10013913A

; Publication No. US20030083462A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James



; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C40  
; CURRENT APPLICATION NUMBER: US/10/013,913A  
; CURRENT FILING DATE: 2002-07-15  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 281  
; LENGTH: 2320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-913A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
        |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
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Db    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

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Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

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Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAAGTTTCAATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAAGTTTCAATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

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Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

Search completed: May 16, 2004, 14:28:50  
Job time : 1403 secs